OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: December 5, 2005, 12:30:01 ; Search time 15657 Seconds
                                        (without alignments)
                                        11505.199 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtcgctgcgaccatgag.............atttctcaatccagaggaag 3169
Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0
Searched: 5883141 seqs, 2842172565 residues
Version
Keywords
Word size :   110
Total number of hits satisfying chosen parameters: 9
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
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                6: gb_pat:*
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                11: gb_sy:*
                12: gb_uni:*
                13: gb_vi:*
                14: gb_htg:*
                15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
c 1	3169	100.0	3169	8	AF417580	AF417580 Homo sapi
c 2	602	19.0	159272	8	HSDJ686C3	AL049712 Human DNA

c	3	493	15.6	2560	6	AX833218	AX833218 Sequence
c	4	493	15.6	2560	8	AK094789	AK094789 Homo sapi
c	5	308	9.7	3566	6	CQ850588	CQ850588 Sequence
c	6	308	9.7	3566	6	AK127751	AK127751 Homo sapi
c	7	298	9.4	884	6	CQ728483	CQ728483 Sequence
c	8	144	4.5	321519	14	AL714004	AL714004 Homo sapi
c	9	116	3.7	635	10	HS692H20T	AL034506 H.sapiens

ALIGNMENTS

RESULT 1
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LOCUS   AF417580   3169 bp   mRNA   linear   PRI 05-MAR-2003
DEFINITION Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA,
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ACCESSION   AF417580
VERSION   AF417580.2 GI:28642834
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 3169)
  AUTHORS   Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
            Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
            Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S.,
            Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F.,
            Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
  TITLE   Dominant and recessive deafness caused by mutations of a novel
            gene, TMC1, required for cochlear hair-cell function
  JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
  PUBMED   11850618
REFERENCE   2 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
REFERENCE   3 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
REMARK   Sequence update by submitter
COMMENT   On Mar 3, 2003 this sequence version replaced gi:19223982.
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ORIGIN
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Qy       121 TCAAGCAAGCGGGGCCTCTCAAAGCGGCGAGGGGACCCCAGGCAGGCGGGAGCTCAGCGAAGC 180
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Qy       241 CCCAGGAGACACAGAGAAAGAGCTGGGGGACCACGGCGGGGGCCGAGGAGGAGGACCTGC 300
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Db       241 CCCAGGAGACACAGAGAAAGAGCTGGGGGACCACGGCGGGGGCCGAGGAGGAGGACCTGC 300

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Qy       421 TCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGGGACTCCCTGTCCCGGAGGAGGAGAACTGGCCCAG 480
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Qy       781 CTCCGGATGGATGTATGGAGTTAACCTTGTCCTTTTTGGGCTTAATATTGGTCTAGTCATA 840
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Qy       841 ATCCCAGAGGTACTGATGGGCCATGCCCTATGGGAGTATTCCCAGAAGACAGTGCCTCGG 900
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Qy       901 GCTGAGGAAGAAAAGGCCATGGATTTTTCTGTCCTTTGGGATTTTGAGGGCTATATCAAG 960
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Qy       961 TACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGGATCATCGGGTGGCTGAGGTAC 1020
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Qy      1081 GTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGGGGAGGGAGAGTCGACAAC 1140
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Qy   1741 GAGACAGACTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACATGCTTGGTAACGTAC 1800
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RESULT 2

LOCUS   HSDJ686C3/c
HSDJ686C3   159272 bp   DNA   linear   PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP4-686C3 on chromosome 20 Contains
            the IDH3B gene for isocitrate dehydrogenase 3 (56kDa with KKE/D repeat), the
            NOL5A gene for nucleolar protein 5A (56kDa with KKE/D repeat), the
            TMC2 gene for transmembrane cochlear expressed protein 2, a novel
            gene, the RNU56 gene for small nuclear RNA U56, the RNU57 gene for
            small nuclear RNA U57, the 5' end of one variant of the ZNF343 gene
            for zinc finger protein 343 and three CpG islands, complete
            sequence.
ACCESSION   AL049712
VERSION   AL049712.12 GI:5629919
KEYWORDS   HTG; C20orf145; CpG island; FLJ37470; IDH3B; isocitrate
            dehydrogenase 3; NOL5A; NOP56; nucleolar protein 5A; RNU56; RNU57;
            small nuclear RNA; TMC2; ZNF343.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 159272)
  AUTHORS   Smith,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequests@sanger.ac.uk
COMMENT   On Jul 28, 1999 this sequence version replaced gi:5578962.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 20, constructed by the Sanger Centre Chromosome 20
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr20
            RP4-686C3 is from the library RPCI-4 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            -------------- Genome Center
            VECTOR: pCYPAC2
            Center: Wellcome Trust Sanger Institute
            Center code: SC

Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

FEATURES   Location/Qualifiers
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gene   H68937
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Best Local Similarity   99.8%;   Pred. No.; 0;
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Qy   2517 AGAGACACTCCTCCCTCTGCCAGCCAAAGCCCAGGCCCATGGACAACAAGAAGAGGCCCAGGCGGCCC 2576
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Db 30817 AGAGACCACTCCTCCCTCTGCCAGCCAAAGCCCAGGCCCATGGACAACAAGAAGAGGCCCAGGCGGCCC 30758

Qy   2577 TGGGACCTTCCAATTCTGCCAGCAGGACGACCACACTGCCTGCCTCTGGACACCTTCCTATATC 2636
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Db 30757 TGGGACCTTCCAATTCTGCCAGCAGGACGACCACACTGCCTGCCTCTGGACACCTTCCTATATC 30698

RESULT 3

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LOCUS       AX833218                2560 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 342 from Patent EP1347046.
ACCESSION   AX833218
VERSION     AX833218.1  GI:39919353
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1347046-A 342 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1..2560
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ORIGIN
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Query Match   15.6%; Score 493; DB 6; Length 2560;
Best Local Similarity 99.7%; Pred. No. 7e-272;
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Db  30697 TCGGCCCCTGGAATCGGACCACGAGATTCTGCCACGGCCCATCTCAGACTCATCCGTGGAG 30638

Qy   2697 GTCAGCCTCTGGAAAGAGTGCTCAGAGACTCAGGGACCTAGGACTCATCCGTGGAGGAGC 2756
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Db  30637 GTCAGCCTCTGGAAAGAGTGCTCAGAGACTCAGGGACCTAGGACTCATCCGTGGAGGAGC 30578

Qy   2757 CTCGACCCTAGGGCTGATCCTCAAGTACCCCAGTTTCACACATTACCAAACCAAGGTTCTC 2816
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Db  30577 CTCGACCCTAGGGCTGATCCTCAAGTACCCCAGTTTCACACATTACCAAACCAAGGTTCTC 30518

Qy   2817 TCCCCTCTTCCTCTCACATACATGCTCTCTCCTCTTGGAATGCATGAACTTTGAT 2876
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Qy   2937 GAAGCTGGAGCCAATCTCTCGCACTAACTGCCCTCCCAAAATATCTTGGTTCAGACAGCTCTG 2996
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Db  30397 GAAGCTGGAGCCATCTCTCGCACTAACTGCCCTCCCAAAATATCTTGGTTCAGACAGCTCTG 30338

Qy   2997 AACCCACCGCTCACGTGGTCGACCTTGCCTCCCGATTTCGGAGTTGGGGAAGGGCCAT 3056
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Db  30337 AACCCCACCGCTCACGTGGTCGACCTTGCCTCCCGATTTCGGAGTTGGGGAAGGGCCAT 30278

Qy   3057 GACCACCTCGTGTAGACTTTTTCCATGGGATACAGTTTAGGACAGCGGGTTTCTCCGCAGCTT 3116
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  30277 GACCACCTCGTGTAGACTTTTTCCATGGGATACAGTTTAGGACAGCGGGTTTCTCCGCAGCTT 30218

Qy   3117 CCCTAACCAAGGAGGAGGGATGGGAGAAGGGGCCTACATTTCTCAATCCAGAGGAAG 3169
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RESULT 4

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LOCUS       AK094789                2560 bp    mRNA    linear   PRI 30-JAN-2004
DEFINITION  Homo sapiens cDNA FLJ37470 fis, clone BRAWH2012258.
ACCESSION   AK094789
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Qy   1293 AAGATTCTTCGTGTCCTTGGCCAACTTTCTCATCATCTGCGTTTGTTGGAAGTGGGTA 1352
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Db      1 AAGATTCTTCGTGTCCTTGGCCAACTTTCTCATCATCTGCGTTTGTTGGAAGTGGGTA 60

Qy   1353 CCTCATTTACTTTGTGGTTAAGCCGATCTCAGCGAATTCTCCAAAATGCAGAATGTCAGCTG 1412
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Qy   1413 GTATGAAAGGAATGAGGTTAGAGATCGTGATGTGTCCCTGCTTGGAATGTTTTGTCCCCCCT 1472
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Qy   1473 GTTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACCGCACTGACTGAAGTGGCCAGCT 1532
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VERSION   AK094769.1 GI:21753918
KEYWORDS   oligo capping; fls (full insert sequence).
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
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            Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE   Complete sequencing and characterization of 21,243 full-length
            human cDNAs
JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
PUBMED   14702039
REFERENCE   2
AUTHORS   Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
            Shiohata,N., Matsumoto,K., Matsumoto,K., Sano,S., Nomura,R.,
            Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
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            Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,
            Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
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            Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 2560)

AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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ORIGIN

Query Match   15.6%; Score 493; DB 8; Length 2560;
Best Local Similarity   99.7%; Pred. No. 7e-272;
Matches 593; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy   1353 CCTCATTTACTTTGTGGTTAAGCGATCTCAGCAANTTCTCCAAAATGCAGAATGTCAGCTG 1412
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Db   121 GTATGAAAGGAATGAGGTAGAGATCGTGATGTCCCTGGCTGGTGGAATGTTTGTCCCCTCT 180

Qy   1473 GTTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACCCACTGGACTGGAAGTGGCAGCT 1532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACCCACTGGACTGGAAGTGGCAGCT 240

Qy   1533 GGGAGCAGCATCTTGCACTCTTCCTGGGGAACCTCTACACATTTCTTGGCCCTGATGA 1592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GGGAGCAGCATCTTGCACTCTTCCTGGGGAACCTCTACACATTTCTTGGCCCTGATGGA 300

Qy   1593 TGACGTCCACCTCAAGCTTGCTAATGAAGAGACAAATAAAGAAGACATCACTCACTGGACTCT 1652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGATGTCCACCTCAAGCTTGCTAATGAAGAGACAAATAAAGAAGACATCACTCACTGGACTCT 360

Qy   1653 GTTTAACTATTACAACTCTTCTGTTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCC 1712
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTTAACTATTACAACTCTTCTGTTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCC 420

Qy   1713 TGCAGAGTGTCCCCCGGGGGGTTCTTGCTCGGGGATGACAGCTGTGGGGCATTGAATTCATGAGGCT 1772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGCAGAGTGTCCCCCGGGGGGTTCTTGCTCGGGGATGACAGCTGTGGGGCATTGAATTCATGAGGCT 480

Qy   1773 GACGGTGTCTGACACATGCTGGTAAGGTAACATCACTACATCACCATTCCTGCTGGGGGACTTCCTACGGGC 1832
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GACGGTGTCCGACACATGCTGGTAACGTAACATCACCATTCCTGCTGGGGGACTTCCTACGGGC 540

Qy   1833 TTGTTTTGTGCCGGTTCATGAACTACTCCTGGTGCTGGGGACTTGGAGGCTGGATTT 1887
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Db   541 TTGTTTTGTGCCGGTTCATGAACTACTCCTGGTGCTGGGGACTTGGAGGCTGGATTT 595

RESULT 5
CQ850588
LOCUS   CQ850588   3566 bp   DNA   linear   PAT 23-AUG-2004
DEFINITION Sequence 1057 from Patent EP1447413.
ACCESSION   CQ850588
VERSION   CQ850588.1 GI:51508800
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
            Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
  TITLE   Full-length human cDNA
  JOURNAL   Patent: EP 1447413-A 1057 18-AUG-2004;
            Research Association for Biotechnology (JP)
FEATURES   Location/Qualifiers
     source   1..3566
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   9.7%; Score 308; DB 6; Length 3566;
Best Local Similarity   100.0%; Pred. No. 5.4e-165;
Matches 308; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1888 CCTTCATATCCTGAGTTTGATATTAGTTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGA 1947
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Db   163 CCTTCATATCCTGAGTTTGATATTAGTTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGA 222

Qy   1948 ATGATCTGGATGGGCTCCTTCATGCTCCAGGCCTGGGGCATTAATGTGCTCGGGCCTG 2007
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Db   223 ATGATCTGGATGGGCTCCTTCATGCTCCAGGCCTGTGGTGGGCATTAATGTGCTCGGGCCTG 282

Qy   2008 CTGACCTCCATGTACTTCCAGTGTGCTGGGGGGGGTGATGAGCAGCAAACGTACCCGATGAAACGC 2067
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Db   283 CTGACCTCCATGTACTTCCAGTGTGCTGGGGGGGTGATGAGCAGCAAACGTACCCGATGAAACGC 342

Qy   2068 GTGTTCAAAGCCTCCCGGATCCAACGAACTTCTACATGGGCGCTCCTGCTGCTGGTGCTTC 2127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   343 GTGTTCAAAGCCTCCCGGATCCAACGAACTTCTACATGGGCGCTCCTGCTGCTGGTGCTTC 402

Qy   2128 CTCAGCCTCCTGCCGGGTGGCCTACACCATCATGTCCCTCCCACACCTCCTTTGACTGCGGG 2187
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 CTCAGCCTCCTGCCGGGTGGCCTACACCATCATGTCCCTCCCACACCTCCTTTGACTGCGGGG 462

Qy   2188 CCGGTTCAG 2195
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Db   463 CCGGTTCAG 470

RESULT 6
AK127751
LOCUS   AK127751   3566 bp   mRNA   linear   PRI 19-FEB-2004
DEFINITION Homo sapiens cDNA FLJ45851 fis, clone OCBBF2018229.
ACCESSION   AK127751
VERSION   AK127751.1 GI:34534796
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
            Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
            Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
            Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
            Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE   NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 3566)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE   Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: Reverse Proteomics Research Institute, HRI and
            RAB.

FEATURES   Location/Qualifiers

source   1..3566
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                 /clone="OCBBF2018229"
                 /tissue_type="brain"
                 /clone_lib="OCBBF2"
                 /dev_stage="fetal"
                 /note="cloning vector: pME18SFL3"

CDS   223..711
                 /note="unnamed protein product"
                 /codon_start=1
                 /db_xref="GI:3454797"
                 /protein_id="BAC87114.1"
                 /translation="MIWMGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPHERVFKA
                 SRSNNYYMGLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRG
                 PRPIPVLVSCQPVKGHGTLGESPMPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVEC
                 LK"

ORIGIN

Query Match   9.7%;   Score 308;   DB 8;   Length 3566;
Best Local Similarity   100.0%;   Pred. No. 5.4e-165;
Matches   308;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1888 CCTTCATATCCTGAGTTTGATAATTAGTGGAAAATGTGCTGGGTTTGATCTTCAACCAAGGA 1947
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   163 CCTTCATATGCTGAGTTTGATAATTAGTGGAAAATGTGCTGGGTTTGATCTTCAACCAAGGA 222

Qy   1948 ATGATCTGGATGGGCTCCTTCTATGCTCATGCCAGGCCTGGTGGGCATTAATGTCCTCGCCCTG 2007
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   223 ATGATCTGGATGGGCTCCTTCTATGCTCATGCCAGGCCTGGTGGGCATTAATGTCCTCGCCCTG 282

Qy   2008 CTGACCTCCATGTACTTCCAGTGCTGGGCGGGTGATGAGCAGCAAGCGTACCCCATGAACGC 2067
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   283 CTGACCTCCATGTACTTCCAGTGCTGGGCGGGTGATGAGCAGCAAGCGTACCCCATGAACGC 342

Qy   2068 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCGCTCCTGCTGGTGCTCTTC 2127
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   343 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCGCTCCTGCTGGTGCTCTTC 402

Qy   2128 CTCAGGCCTCCTGCCGGTGGCCTACACCACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGG 2187
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 CTCAGGCCTCCTGCCGGTGGCCTACACCACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGG 462

Qy   2188 CCGTTCAG 2195
             ||||||||
Db   463 CCGTTCAG 470

RESULT 7
CQ728483

LOCUS   CQ728483   884 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 14417 from Patent WO02068579.
ACCESSION   CQ728483
VERSION   CQ728483.1   GI:42297418
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W., and Myers,E.W.
  TITLE   Kits, such as nucleic acid arrays, comprising a majority of
                humanexons or transcripts, for detecting expression and other uses
                thereof
  JOURNAL   Patent: WO 02068579-A 14417 06-SEP-2002;
                PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
source   1..884
                 /organism="Homo sapiens"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:9606"
ORIGIN

Query Match   9.4%;   Score 298;   DB 6;   Length 884;
Best Local Similarity   100.0%;   Pred. No. 3e-159;
Matches   298;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   946 GAGGGCTATATCAAGTACTCCTCCACTCTTCTATGGCTACTACAACACCAACCAGAGGACCATC 1005
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187 GAGGGCTATATCAAGTACTCCTCCACTCTTCTATGGCTACTACAACACCAACCAGAGGACCATC 246

Qy   1006 GGGTGGCTGAGGTACCCGCCTCCCTATGCCTATGGCTTACTTTATGGGGGCGGGGTCAGCCTGGC 1065
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Db   247 GGGTGGCTGAGGTACCCGCCTCCCTATGCCTATGGCTTACTTTATGCGTGGGGGGTCAGCGTGTTCGGC 306

Qy   1066 TACAGCCTGATTATTGTCATTCGATCGATGGCCGCAATACCCAAGGAAGCACAGGCGAA 1125
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Db   307 TACAGCCTGATTATTGTCATTCGATCGATGGCCGCAATACCCAAGGAAGCACAGGCGAA 366

Qy   1126 GGGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCCAGCTGGGGACTACCTGATC 1185
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Db   367 GGGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCCAGCTGGGGACTACCTGATC 426

Qy   1186 GGGAATTCAGAGACAGCGTGATAACAAATATCATCACCACCACCACCAGCTTCAAGGAAT 1243
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Db   427 GGGAATTCAGAGACAGCTGATAACGAAATATGCATCATCACCACCACCACCAGCTTCAAGGAAT 484

RESULT 8
AL714004/c

LOCUS   AL714004   321519 bp   DNA   linear   HTG 21-MAY-2002
DEFINITION   Homo sapiens clone XX-CHR_20-17119-3, *** SEQUENCING IN PROGRESS
                ***, 89 unordered pieces.
ACCESSION   AL714004
VERSION   AL714004.35   GI:21104209
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE   1 (bases 1 to 321519)
  AUTHORS   Plumb,B.
  TITLE   Direct Submission
  JOURNAL   Submitted (20-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT   On May 22, 2002 this sequence version replaced gi:21068608.

            -------------- Genome Center

            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information

            Center project name: Chr_20-17119-3
            -------------- Summary Statistics

            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator; 100% of reads
            Consensus quality: 254683 bases at least Q40
            Consensus quality: 281730 bases at least Q30
            Consensus quality: 299177 bases at least Q20
            Insert size: 312719; sum-of-contigs
            Quality coverage: 1.63x in Q20 bases; sum-of-contigs

            ----
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 89 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
          *   1 4746: contig of 4746 bp in length
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          *   7273 9289: contig of 2017 bp in length
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          *   9390 11807: contig of 2418 bp in length
          *   11808 11907: gap of 100 bp
          *   11908 13962: contig of 2055 bp in length
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          *   14063 16347: contig of 2285 bp in length
          *   16348 16447: gap of 100 bp
          *   16448 18532: contig of 2085 bp in length
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          *   20655 20754: gap of 100 bp
          *   20755 23021: contig of 2267 bp in length
          *   23022 23121: gap of 100 bp
          *   23122 25134: contig of 2013 bp in length
          *   25135 25234: gap of 100 bp
          *   25235 28284: contig of 3051 bp in length
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          *   28385 30541: contig of 2157 bp in length
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          *   35600 35699: gap of 100 bp
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          *   55473 58397: contig of 2926 bp in length
          *   58399 58498: gap of 100 bp
          *   58499 61833: contig of 3336 bp in length
          *   61835 61934: gap of 100 bp
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          *   122034 122133: gap of 100 bp
          *   122134 124238: contig of 2105 bp in length
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178421 178520: gap of 100 bp
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184023 184122: gap of 100 bp
184123 186233: contig of 2111 bp in length
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190935 193769: contig of 2835 bp in length
193770 193869: gap of 100 bp
193870 196119: contig of 2250 bp in length
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196220 200732: contig of 4513 bp in length
200733 200832: gap of 100 bp
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204194 206520: contig of 2327 bp in length
206521 206620: gap of 100 bp
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208780 210932: contig of 2153 bp in length
210933 211032: gap of 100 bp
211033 213133: contig of 2101 bp in length
213134 213233: gap of 100 bp
213234 217420: contig of 4187 bp in length
217421 217520: gap of 100 bp
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222146 222245: gap of 100 bp
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236634 239252: contig of 2619 bp in length
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255512 258118: contig of 2607 bp in length
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260852 263142: contig of 2291 bp in length
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270324 274441: contig of 4118 bp in length
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280983 281082: gap of 100 bp
281083 283442: contig of 2360 bp in length

Query Match   4.5%; Score 144; DB 14; Length 321519;
Best Local Similarity 99.5%; Pred. No. 3.8e-70;
Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1237 AAGGAATCAATAGTGGATGAACAAGAGAGTAACAAGAAGAAAATATCCATCTGACAAGA 1296
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Db 317605 AAGGAATCAATAGTCGATGAACAAGAGAGTAACAAGAAGAAAATATCCATCTGACAAGA 317546

Qy   1297 TTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGAGAGTGGGTACCTC 1356
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Db 317545 TTTCTTCGTGTCCTGGCTAACTTTCTCATCATCTGCTGTTTGTGTGAGAGTGGGTACCTC 317486

Qy   1357 ATTTACTTTGTGGTTAAGCGGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTGGTAT 1416
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 317485 ATTTACTTTGTGGTTAAGCGGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTGGTAT 317426

Qy   1417 GAAAGGAATGAGGTA 1431
           |||||||||||||||
Db 317425 GAAAGGAATGAGGTA 317411

RESULT 9
HS692H2OT
LOCUS   HS692H2OT   635 bp   DNA   linear   STS 14-DEC-1998
DEFINITION H.sapiens STS from genomic clone 692H20, sequence tagged site.
ACCESSION   AL034506
VERSION   AL034506.1 GI:4008495
KEYWORDS   STS; single read.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 635)

AUTHORS   Deloukas,P., O'Neill,L., Holden,J., Mistry,D., Huckle,E., Taylor,R.
             and Hunt,S.
TITLE   Direct Submission
JOURNAL   Submitted (14-DEC-1998) E-mail contact: humquery@sanger.ac.uk
COMMENT   Marker std J692H2OT7 (Primer A : AATGAAGGAGGAAAAGAAGGGG; Primer B :
             GGTAAGCTCAGAGCTGGGTGG; amplimer size : 176 bp) is from sequence
             generated from the T7 end of PAC 692H20. 692H20 is part of the
             bacterial clone contigs constructed by the Chromosome 20 Mapping
             Group.(http://www.sanger.ac.uk/HGP/Chr20/) 692H20 is from the
             library RPCI4 constructed at the Roswell Park Cancer Institute by
             the group of Pieter de Jong.
             For further details see http://bacpac.med.buffalo.edu/.
FEATURES   Location/Qualifiers
     source   1..635
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="20"
                     /clone="692H20"
ORIGIN

Query Match   3.7%;   Score 116; DB 10; Length 635;
Best Local Similarity 100.0%; Pred. No. 4.2e-54;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   947 AGGGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACACAACCAGAGGACCATCG 1006
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   520 AGGGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACACAACCAGAGGACCATCG 579

Qy   1007 GGTGGCTGAGGTACCCGGCTGCCTATGGCTTACTTTATTGGTGGGGGTCAGCCGTGTTC 1062
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   580 GGTGGCTGAGGTACCCGGCTGCCTATGGCTTACTTTATTGGTGGGGGTCAGCCGTGTTC 635

Search completed: December 6, 2005, 03:55:58
Job time : 15660 secs

                                                    GenCore version 5.1.6
                                              Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 09:34:11 ; Search time 1705 seconds
                                               (without alignments)
                                               12387.338 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgtcgaccatgag.........atttcctcaatccagaggaag 3169

Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size :   110

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_21
                1: geneseqn1980s:*
                2: geneseqn19905:*
                3: geneseqn2000s:*
                4: geneseqn2001as:*
                5: geneseqn2001bs:*
                6: geneseqn2002as:*
                7: geneseqn2002bs:*
                8: geneseqn2003as:*
                9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
                14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result   Query
No.   Score Match Length DB ID   Description
------ ----- ----- ------ -- ---------   -----------
1   3074   97.0 3121   8   ACC69614   Acc69614 Human tra
2   1750   55.2 5027   5   AAS92296   Aas92296 DNA encod
3   493   15.6 2560   11 ADM01657   Adm01657 Human cDN
4   359   11.3 2591   6   ABV75613   Abv75613 Human rib

RESULT 1

ACC69614

5   308   9.7   3566   13   ADR07551   Adr07551 Full leng

ID   ACC69614 standard; cDNA; 3121 BP.
XX
AC   ACC69614;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Human transduction-2 (TDC2) encoding cDNA SEQ ID NO:3.
XX
KW   Human; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   CDS   16..2688
FT   /tag= a
FT   /product= "transductin-2"
XX
PN   WO200302514O-A2.
XX
PD   27-MAR-2003.
XX
PF   19-SEP-2002; 2002WO-US029614.
XX
PR   19-SEP-2001; 2001US-0323275P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Griffith AJ, Kurima K, Wilcox E, Friedman T;
XX
DR   WPI; 2003-371806/35.
DR   P-PSDB; ABR43616.
XX
PT   An isolated or purified nucleic acid molecule encoding transductin-1
PT   (TDC1), TDC2, or its fragment, useful for prognosticating, treating or
PT   monitoring hearing loss.
XX
PS   Claim 9; Fig 2; 85pp; English.
XX

CC   The present sequence encodes human transductin-2 (TDC2). The present
CC   invention describes human and mouse TDC1 and TDC2. Also described: (1) a
CC   method for detecting hearing loss or predisposition to hearing loss in an
CC   animal; (2) a method for determining the level of nucleic acid comprising
CC   wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
CC   sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
CC   gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
CC   method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
CC   TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
CC   type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
CC   comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
CC   and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
CC   for treating an animal prophylactically or therapeutically for hearing
CC   loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
CC   a method for identifying one or more agents that interact with a TDC1
CC   and/or TDC2 genes in a cell by administering one or more agents to the
CC   cell comprising the genes and assaying the expression level of the genes
CC   by the cell, where an increase or decrease in the expression level is
CC   indicative of the interaction between the agents and the genes in the
CC   cell. TDC1 and TDC2 have auditory activities and can be used in gene
CC   therapy. The molecules, compositions and methods of the present invention
CC   can be used for prognosticating, treating and monitoring hearing loss
XX
SQ   Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

Query Match   97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3074; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   96 AGGTGACAAGGCCTGGGAAGGAGATCCTCAAGCAAGCGGGGCTCTCAAAGCCGAGGGAACCC 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   48 AGGTGACAAGGCCTGGGAAGGAGATCCTCAAGCAAGCGGGGCTCTCAAAGCCGAGGGAACCC 107

Qy   156 AGGCAGGGCGCCGGAGCTCAGCCGAAGGCCAGAAGCCGCGCCGGGGGCCAGCCCAAGCCCCGG 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 AGGCAGGGCGCCGGAGCTCAGCCGAAGGCCAGAAGCCGCGCCGGGGGCCAGCCCAAGCCCCGG 167

Qy   216 GTCTCCCCGGAGGAGAAGCAAAACAGGGGCGGCAGGAGCACAGAGAAGCAGACTCGGGGGAGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   168 GTCTCCCCGGAGGAGAAGCAAAACAGGGGCGGCAGGAGCACAGAGAAGCAGACTCGGGGGAGGA 227

Qy   276 GCGGGGGCCAGGCGAGAGAGGAGGGCCAGGGCCAGGAGACAGAAAGCCGCACGCAGAGGCCTCCTT 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 GCGGGGGCCAGGCGAGAGAGGAGGGCCAGGGCCAGGAGACAGAAAGCCGCACGCAGAGGCCTCCTT 287

Qy   336 CCAGGAGCGGCAGCAGCGCCCCAAAGAGGGAAAAGGAGATTCCGAGGAAGGAGGAGAAGTC 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   288 CCAGGAGCGGCAGCAGCGCCCCAAAGAGGGAAAAGGAGATTCCGAGGAAGGAGGAGAAGTC 347

Qy   396 GAAGCGGCAGAAGAAAACCCAGGTCATCCTCCTTCGGCCTCCAGTGCCTCTCGGTGGGGAGTC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   348 GAAGCGGCAGAAGAAAACCCAGGTCATCCTCCTTCGGCCTCCAGTGCCTCTCGGTGGGGAGTC 407

Qy   456 CCTGTCCGAGGAGGAACTGGCCCAGATCCTGGACGAGTGGGAGAGAAAAAGAAGCTCAT 515
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Qy   516 TGCCACCATGCGGACCAAGCCCTGCCGAAGGAAGCTGACAGAGCCTCAGGGAGGC 575
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Db   468 TGCCACCATGCGGACCAAGCCCTGCCGAAGGAAGCTGACAGAGCCTCAGGGAGGC 527

Qy   576 CCAGGAATTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAGGGGAAAGGCCAAGCAACTATA 635
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Db   528 CCAGGAATTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAGGGGAAAGGCCAAGCAACTATA 587

Qy   636 TGCCTACAAGATGCTGATGGGCCAAGAAATGGGTCAAATTTAAGAGAGACTTTGATAAATT 695
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```
Db   588  TGCCTACACAGATCGTGATGGCCAAGAAATGGGTCAAATTTAAGAGAACTTTGATAATTT  647

Qy   696  CAAGACTCAATGTATCCCCTGGGAAATGAAGATGAAGGACATTGAAAGTCACTTTGGTTC  755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648  CAAGACTCAATGTATCCCCTGGGAAATGAAGATGAAGGACATTGAAAGTCACTTTGGTTC  707

Qy   756  TTCAGTGGCATCGTATTTCATCTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTT  815
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Db   708  TTCAGTGGCATCGTATTTCATCTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTT  767

Qy   816  TGGCTTAAATATTTGGTCTAGTCATTAATCCCAGAGGTACTGATGGGCATGGGCCATGGGGAG  875
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Db   768  TGGCTTAAATATTTGGTCTAGTCATTAATCCCAGAGGTACTGATGGGCATGGGCCATGGGGAG  827

Qy   876  TATTCCCAGAAAAGACAGTGCCTCGGGCCTGAGGAAGAAAGGCCATGGATTTTTCTGTCCT  935
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Db   828  TATTCCCAGAAAAGACAGTGCCTCGGGCCTGAGGAAGAAAGGCCATGGATTTTTCTGTCCT  887

Qy   936  TTGGGATTTTGAGGGGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACAACAACCA  995
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Db   888  TTGGGATTTTGAGGGGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACAACAACCA  947

Qy   996  GAGGACCACATCGGGTGCTGAGGTACCGGGCTGCCTATGGGGGGGTCAG  1055
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   948  GAGGACCACATCGGGTGCTGAGGTACCGGGCTGCCTATGGGGGGGTCAG  1007

Qy   1056 CGTGTTCGGCTACAGCCTGACTTATTGTCATTCGATCCGATGGCCAGCAAATACCAAGGAAG  1115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 CGTGTTCGGCTACAGCCTGACTTATTGTCATTCGATCCGATGGCCAGCAAATACCAAGGAAG  1067

Qy   1116 CACAGGCGAAGGGAGGAGAGTGACAACTTCACATTCAGCTTCAAGATTGTTCACCAGCTGGGA  1175
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Db   1068 CACAGGCGAAGGGAGGAGAGTGACAACTTCACATTCAGCTTCAAGATTGTTCACCAGCTGGGA  1127

Qy   1176 CTACCTGATCGGGGAAATTCAGAGACGCTGATAACAGATCAGCTGATAACAGATACATCATCCA  1235
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Db   1128 CTACCTGATCGGGGAAATTCAGAGACGCTGATAACAGATCAGCTGATAACAGATACATCATCCA  1187

Qy   1236 CAAGGAATCAATAGTGGATGAACAGAGGAGTAACAAGAAGAGAAAATATCCATCTGACAAG  1295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1188 CAAGGAATCAATAGTGGATGAACAGAGGAGTAACAAGAAGAGAAAATATCCATCTGACAAG  1247

Qy   1296 ATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGGTACCT  1355
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Db   1248 ATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGGTACCT  1307

Qy   1356 CATTTACTTTGTGTGGTTAAACGGATCTCAGCGAATCTCCAAAAATGCAGAATGTCAGCTGGTA  1415
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Qy   1596 CGTCCACCTCAAGCTTGCTAATGAAGGACAATAAAGAGAACATCACTCACTGGACTCTGTT  1655
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Db   1548 CGTCCACCTCAAGCTTGCTAATGAAGGACAATAAAGAGAACATCACTCACTGGACTCTGTT  1607

Qy   1656 TAACTATTACAACTCTTCTGGTTGGAACCGAGAGGTGTCCCCGACCCAACCCTGACCCTGC  1715
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Db   1608 TAACTATTACAACTCTTCTGGTTGGAACCGAGAGGTGTCCCCGACCCAACCCTGACCCTGC  1667

Qy   1716 AGATGTGCCCCGGGGTTCTTGCTGGGGACAGCTGTGGGCCATTGAATTCATGAGGCTGAC  1775
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Db   1668 AGATGTGCCCCGGGGTTCTTGCTGGGGACAGCTGTGGGCCATTGAATTCATGAGGCTGAC  1727

Qy   1776 GGTGTCTGACATGCTGGGTAAGGTACATCACCATCCTGCTGCTGGGGGACTCCTACGGGCTTG  1835
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Qy   1836 TTTTGTGCGGTTCATGAACTACTGCTGGTGGTGCTGGGGAGTTGGGAGCTGGATTTCCTTCATA  1895
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1788 TTTTGTGCGGTTCATGAACTACTGCTGGTGGTGCTGGGGAGTTGGGAGCTGGATTTCCTTCATA  1847

Qy   1896 TGCTGAGTTTGATATTAGTGGAAATGTGCTGCTGGTTTGATCTTCAACCAAGGAATGATCTG  1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1848 TGCTGAGTTTGATATTAGTGGAAATGTGCTGCTGGTTTGATCTTCAACCAAGGAATGATCTG  1907

Qy   1956 GATGGGCTCCTTCTATGCTCCAGGCCGCCTGGTGGGGCATTAATGTGCTCGCGCCTGCTGACCTC  2015
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1908 GATGGGCTCCTTCTATGCTCCAGGCCGCCTGGTGGGGCATTAATGTGCTCGCGCCTGCTGACCTC  1967

Qy   2016 CATGTACTTCCAGTCGTGCTGGGGCGGTGATGAGCAGCAACGTGACCCCATGGAACGCCTGTTCAA  2075
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1968 CATGTACTTCCAGTCGTGCTGGGGCGGTGATGAGCAGCAACGTGACCCCATGGAACGCCTGTTCAA  2027

Qy   2076 AGCCTCCGATCCAACACTCTCACATGGGCCTCCTGCTGGTGTGCTCTTCCTCAGCCT  2135
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Db   2028 AGCCTCCGATCCAACACTCTCACATGGGCCTCCTGCTGGTGTGCTCTTCCTCAGCCT  2087

Qy   2136 CCTGCGCGGTGGCCTACCACCATCATGTCCCTCCCACCCTCCTTGACTGGCGGGGGCGGTTCAG  2195
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Db   2088 CCTGCGCGGTGGCCTACCACCATCATGTCCCTCCCACCCTCCTTGACTGGCGGGGGCGGTTCAG  2147

Qy   2196 TGGGAAAACAGAATGTACGGATGTCCTCCAAGAGACCCATTGAAAACGAATTCCCAACTT  2255
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148 TGGGAAAACAGAATGTACGGATGTCCTCCAAGAGACCCATTGAAAACGAATTCCCAACTT  2207

Qy   2256 CCTGGGCAAGAGATCTTTGCTTTCCTGCGCCAAATCCAGGCGCCTGATCACATCCCAATCCTGCT  2315
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Db   2208 CCTGGGCAAGAGATCTTTGCTTTCCTGCGCCAAATCCAGGCGCCTGATCACATCCCAATCCTGCT  2267

Qy   2316 GATGTTCTTGGCCATTTACTACCTGAACTCAGTTTCCAAAAAGCCTTTCCGGAGCTAATGC  2375
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268 GATGTTCTTGGCCATTTACTACCTGAACTCAGTTTCCAAAAAGCCTTTCCGGAGCTAAATGC  2327
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Qy  2376 CCAGCTGAGGAAGAAAATCCAAGTGCTCCCGTGAAGTTGAGAAAGAGTCACAAATCTGTAAA 2435
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Db  2328 CCAGCTGAGGAAGAAAATCCAAGTGCTCCCGTGAAGTTGAGAAAGAGTCACAAATCTGTAAA 2387

Qy  2436 AGGCAAAGCCACAGCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAAATGCCAC 2495
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Db  2388 AGGCAAAGCCACAGCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAAATGCCAC 2447

Qy  2496 CCAGCTCCAACTCACCAAGGAAGAGAACCACTCCCTTCCGCAGCCAAAACCCAGGCCCAT 2555
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Qy  2556 GGACAAGAAGGCGGCAGGGCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGC 2615
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Qy  2616 CTCTGGACACCTTCCTTATATCTCGGGCCCCCTGAAATCGGACCAGATTCTGGCCACGCCCC 2675
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Db  2568 CTCTGGACACCTTCCTATATCTCGGGCCCCCTGAAATCGGACCAGATTCTGGCCACGCCCC 2627

Qy  2676 ATCTCAGACTCATCCCGTGGAGGTTCAGCGTCTGGAAAGAGTGCTCAGAGGACCTCCCCACTG 2735
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Qy  2736 ACCGGCTAGGACTCCGAGGAGCCTCGACCCTAGGGCTGATCCTCAAGTACCCCAGTTTCAC 2795
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Db  2688 ACGGGCTAGGACTCCGAGGAGCCTCGACCCTAGGGCTGATCCTCAAGTACCCCAGTTTCAC 2747

Qy  2796 ACATACCAAACCAAGGTTCTCTCCCCTCTTCTCTCTCACATACATGCTCTGTCTGTCTCTC 2855
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Qy  2856 TTGGAATGCATGAACTTTGATTCCTTCAGCCCTTGTCAGCTACCGGAAGGAGGAAGACAG 2915
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Db  2808 TTGGAATGCATGAACTTTGATTCCTTCAGCCCTTGTCAGCTACCGGAAGGAGGAAGACAG 2867

Qy  2916 TGGCTTCACCTGTCCTTTAGGGAAGCTGGAGCCCATCTCTGCCACTCAACTGCCCTCCCAAAT 2975
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Db  2868 TGGCTTCACCTGTCCTTTAGGGAAGCTGGAGCCCATCTCTGCCACTCAACTGCCCTCCCAAAT 2927

Qy  2976 ATCTTGGTTCAGACAGCCTCTGAACCCCACCGGCTCACAGTGGTCGACCTTGCCTCCCGATTT 3035
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Qy  3036 TCCGGAGTTGGGGAAGGGCCATGACCACCCTCGTAGACTTTTTTCCATGGGATACAGTTTAG 3095
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2988 TCCGAGTTGGGGAAGGGCCATGACCACCCTCGTAGACTTTTTTCCATGGGATACAGTTTAG 3047

Qy  3096 GACACGGGGTTTGCCAGCTTCCCTAACCAGGAGGGGGATGGAGAAGGGGCCTACATTTCT 3155
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Db  3048 GACACGGGGTTTCCCAGCTTCCCTAACCAGGAGGGGGATGGAGAAGGGGCCTACATTTCT 3107

Qy  3156 CAATCCAGAGGAAG 3169
         ||||||||||||||
Db  3108 CAATCCAGAGGAAG 3121
```

RESULT 2
AAS92296
ID   AAS92296 standard; cDNA; 5027 BP.
XX
AC   AAS92296;
XX
DT   13-FEB-2002 (first entry)
XX
DE   DNA encoding novel human diagnostic protein #28100.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG28109.
XX
PS   Claim 1; SEQ ID NO 28100; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (III). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (III) and its binding partners are useful in medical imaging
CC   of sites expressing (III). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in

```
Query Match             55.2%;  Score 1750;  DB 5;  Length 5027;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1750;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     947 AGGGCTATATCAAGTACTCTGCAACTCTTCTATGGCTACTACAACCAGAGGACCATCG 1006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1094 AGGGCTATATCAAGTACTCTGCAACTCTTCTATGGCTACTACAACCAGAGGACCATCG 1153

Qy    1007 GGTGGCTGAGGTACCGGCCTGCCTACTTTATGGTGGGGGTCAGGGTGTTCGGGCT 1066
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1154 GGTGGCTGAGGTACCGGCCTGCCTATTTATGGTGGGGGTCAGGGTGTTCGGGCT 1213

Qy    1067 ACAGCCTGATTATTGTCATTCGATCGATGGCCAGCAATACCAAGGAAGGACAGGCGAAG 1126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1214 ACAGCCTGATTATTGTCATTCGATCGATGGCCAGCAATACCAAGGAAGGACAGGCGAAG 1273

Qy    1127 GGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGACTACCTGATCG 1186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1274 GGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGACTACCTGATCG 1333

Qy    1187 GGAATTCAGAGACAGCGTGATAACAAATATGCATCCATCACCACCACCAGCTTCAAGAATCAA 1246
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1334 GGAATTCAGAGACAGCGTGATAACAAATATGCATCCATCACCACCACCAGCTTCAAGAATCAA 1393

Qy    1247 TAGTGGATGAACAAGAGAGTAACAAAAGAGAAAAATATCATCTGACAAGATTTCTTCGTG 1306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1394 TAGTGGATGAACAAGAGAGTAACAAAAGAGAAAAATATCATCTGACAAGATTTCTTCGTG 1453

Qy    1307 TCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTG 1366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1454 TCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTG 1513

Qy    1367 TGGTTAAGCGCATCTCAGCAATTCTCAAAAATGCAGAAATGTCACGTGGTATGAAAGGAATG 1426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1514 TGGTTAAGCGCATCTCAGCAATTCTCCAAAAATGCAGAAATGTCACGTGGTATGAAAGGAATG 1573

Qy    1427 AGGTAGAGATCGTGATGTCCCTGCTTGGGAATGTGTTTTGTCCCCCTCTGTTTGAAACCATCG 1486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1574 AGGTAGAGATCGTGATGTCCCTGCTTGGAATGTGTTTTGTCCCCCTCTGTTTGAAACCATCG 1633

Qy    1487 CTGCCCTGGAGAATTACCACCACCACGGACACTGACTGAAGTGGCAGCTGGGACGCATCTTTG 1546
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1634 CTGCCCTGGAGAATTACCACCACCACGGACTGAAGTGGCAGCTGGGACGCATCTTTG 1693

Qy    1547 CACTCTTCCTGGGGGAACCCTCTACACATTTCTTTGGCCCTGATGGATGAGGTCCACCTCA 1606
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1694 CACTCTTCCTGGGGAACCCTCTACACATTTCTTTGGCCCTGATGGATGAGGTCCACCTCA 1753

Qy    1607 AGCTTGCTAATGAAGAGACAAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACA 1666
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1754 AGCTTGCTAATGAAGAGACAAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACA 1813

Qy    1667 ACTCTTCTGGTTGGGAACCAGAGAGTGTCCCCGGACCACCCTGCACCCTGCAGGATGTGCCCC 1726
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1814 ACTCTTCTGGTTGGGAACCGAGAGTGTCCCCGGACCACCCTGCACCCTGCAGGATGTGCCCC 1873

Qy    1727 GGGGTTCTTGCTGGGGAGCACGCTGTGGGGCATTGTGGGGGCATTCATGAGGGCTGACGGTGTCTGACA 1786
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1874 GGGGTTCTTGCTGCTGGGGAGCACGCTGTGGGGCATTGATTCATGAGGGCTGACGGTGTCTGACA 1933

Qy    1787 TGCTGGTAAGCTACATCAACCATCCTTGCTGGGGGAGCTTCCTACGGGCTTGTTTTGTGCGGGT 1846
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1934 TGCTGGTAAGCTACATCAACCATCCTTGCTGGGGGAGCTTCCTACGGGCTTGTTTTGTGCGGGT 1993

Qy    1847 TCATGAACTACTGCTGCGTGCTGGGAGGCTGGGAGGCTGGATTTCCTTCATATGCTGAGTTTG 1906
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1994 TCATGAACTACTGCTGCGTGCTGGGAGGCTGGGAGGCTGGATTTCATGAGGGCTGAGTTTG 2053

Qy    1907 ATATTAGTGGAAAATGTCGTGGTTTGATCTTCAACCAAGGAATAGATCTGGATGGGGCTCCT 1966
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2054 ATATTAGTGGAAAATGTCGTGGTTTGATCTTCAACCAAGGAATGGATGGGGCTCCT 2113

Qy    1967 TCTATGCTCCAGCGCCTGGTGGGCATTAATGTGCTGCGCCTGCTGCTGCTGACCTCCATGTGTACTTCC 2026
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2114 TCTATGCTCCAGCGCCTGGTGGGCATTAATGTGCTGCGCCTGCTGACCTCCATGTACTTCC 2173

Qy    2027 AGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGCGGTGTTCAAAGCCTCCCGAT 2086
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2174 AGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGCGGTGTTCAAAGCCTCCCGAT 2233

Qy    2087 CCAACAACTTCTACATGGGCCTCTGTCTGCTGGTCTTCCTCCAGCTCCTGCCGGTGG 2146
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2234 CCAACAACTTCTACATGGGCCTCCTGCTGCTGGTCTTCCTCCAGCTCCTGCCGGTGG 2293

Qy    2147 CCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGTGGGAAAAACA 2206
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2294 CCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGTGGGAAAAACA 2353

Qy    2207 GAATGTACGATGTCCTCCAAGAGACCATTGAAAACGGATTCCCAACCTTCCTGGGCAAGA 2266
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2354 GAATGTACGATGTCCTCCAAGAGACCATTGAAAACGGATTCCCAACCTTCCTGGGCAAGA 2413

Qy    2267 TCTTTGCTTTCCTCGCCAATCCAGCCTGATCAATCCCACCACTCTGCTGATGTCTTGG 2326
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2414 TCTTTGCTTCCTCGCCAATCCAGCCTGATCAATCCCACCACTCTGCTGATGTCTTGG 2473

Qy    2327 CCATTACTACCTGAACTCAGTTCCAAAAGCCTTCCCGGACTAATGCCCAGCTGAGGA 2386
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2474 CCATTACTACCTGAACTCAGTTCCAAAAGCCTTCCCGGACTAATGCCCAGCTGAGGA 2533

Qy    2387 AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGTCACAAATCTGTAAAAGGCAAAGCCA 2446
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2534 AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGTCACAAATCTGTAAAAGGCAAAGCCA 2593

Qy    2447 CAGCCAGAGATTCAGAGGACACACCTAAAAGCAGTTCCAAAAAATGCCACCAGCTCCAAC 2506
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2594 CAGCCAGAGATTCAGAGGACACACCTAAAAGCAGTTCCAAAAAATGCCACCAGCTCCAAC 2653

Qy    2507 TCACCAAGGAAGAGAGACCACTCCTCCCTCTGCAGCCAAAGCCAGCCATGGACACAGAAGG 2566
```

Db 2654 TCACCAAGGAAGAGAGACCACTCCTCCCTCTGCCAGCCAAAAGCCAGGCCATGGACAAGAAGG 2713
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 2567 CCGCAGGGGCCCTGGGACCTCCAATTCTCCAGCAGGAGGACCAGACTGCCTGCCTCTGGACACC 2626
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2714 CGCAGGGGCCCTGGGACCTCCAATTCTGCCAGCAGGAGGACCAGACTGCCTGCCTCTGGACACC 2773

Qy 2627 TTCCTATATCTCGGCCCCTGGAATCGGACCACCAGATTCTGGCCACGCGCCCATCTCAGAGCTC 2686
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2774 TTCCTATATCTCGGCCCCTGGAATCGGACCACCAGATTCTGGCCACGCGCCCATCTCAGAGCTC 2833

Qy 2687 ATCCGTGGAG 2696
        ||||||||||
Db 2834 ATCCGTGGAG 2843

RESULT 3
ADM01657
ID ADM01657 standard; cDNA; 2560 BP.
XX
AC ADM01657;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human cDNA of the invention SEQ ID NO:342.
XX
KW gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS Homo sapiens.
OS
XX
PN EP1347046-A1.
XX
PD 24-SEP-2003.
XX
PF 12-APR-2002; 2002EP-00008400.
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR P-PSDB; ADM04100.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 342; 305pp; English.
XX
CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC cDNA sequence of the invention.
XX
SQ Sequence 2560 BP; 568 A; 652 C; 568 G; 772 T; 0 U; 0 Other;

Query Match   15.6%; Score 493; DB 11; Length 2560;
Best Local Similarity   99.7%; Pred. No. 3.2e-226;
Matches 593; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy 1293 AAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCCTGTTTGTGTGGAAGTGGGTA 1352
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCCTGTTTGTGTGGAAGTGGGTA 60

Qy 1353 CCTCATTTACTTTGTGGTTAAGCGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTG 1412
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTCATTTACTTTGTGGTTAAGCGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTG 120

Qy 1413 GTATGAAAAGGAAATGAGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCCTCT 1472
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GTATGAAAAGGAAATGAGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCCTCT 180

Qy 1473 GTTTGAAACCATCGGTGCCCTGGAGAATTACCACCCACGCCACTGGACTGAAGTGGCGAGCT 1532
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GTTTGAAACCATCGGTGCCCTGGAGAATTACCACCCACGCCACTGGACTGAAGTGGCGAGCT 240

Qy 1533 GGGACGGCATCTTCGCACTTCCTGGGGAACCTCTACACACATTTCTCTTGGCCCTGATGGA 1592
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GGGACGGCATCTTCGCACTTCCTGGGGAAACCTCTACACACATTTCTCTTGGCCCTGATGGA 300

Qy 1593 TGACGTCCACCTCAAGCTTGCTAATGAACGTAATAAAGAAGAACATCACTCACTGGACTCT 1652
        ||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 301 TGATGTCCACCTCAAGCTTGCTAATGAAGAGACAATAAAGAAGAACATCACTCACTGGACTCT 360

Qy 1653 GTTTAACTATTACAACTCTTCTGGTTGGAACGGAGAGTGTCCCCCGACCACCCCTGCACCC 1712
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GTTTAACTATTACAACTCTTCTGGTTGGAACGGAGAGTGTCCCCCGACCACCCCTGCACCC 420

Qy 1713 TGCAGAGTGCCCCGGGGTTCTTGCTGGGAGACAGCCTGTGGGCATTGAATTCATGAGGCT 1772
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 TGCAGAGTGCCCCGGGGTTCTTGCTGGGAGACAGCCTGTGGGCATTGAATTCATGAGGCT 480

Qy 1773 GACGGGTGCTGACATGCTGGTAAGCTGCATCATCACCATCCTGCTGGGGGGACTTCCTACGGGC 1832
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GACGGGTGCCGACATGCTGGTAAGCTGCATCATCACCATCCTGCTGGGGGGACTTCCTACGGGC 540

Qy 1833 TTGTTTGTTGCGGTTCATGAACTACTGCTGGTTGCTGGGACTTGGAGGCTGGGATTT 1887
        ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TTGTTTTGTTGCGGTTCATGAACTACTGCTGGTTGCTGGGACTTGGAGGCTGGGATTT 595

RESULT 4
ABV75613
ID ABV75613 standard; cDNA; 2591 BP.

XX
AC   ABV75613;
XX
DT   23-JAN-2003 (first entry)
XX
DE   Human ribosomal protein L3220.9 cDNA.
XX
KW   Human; ribosomal protein L3220.9; diabetes; menstrual disorder; anaemia;
KW   peptic ulcer; arrhythmia; epilepsy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   74..646
FT   /tag= a
FT   /product= "Ribosomal protein L3220.9"
XX
PN   CN1345827-A.
XX
PD   24-APR-2002.
XX
PF   29-SEP-2000; 2000CN-00125511.
XX
PR   29-SEP-2000; 2000CN-00125511.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y, Xie Y;
XX
DR   WPI; 2002-548952/59.
DR   P-PSDB; ABP57746.
XX
PT   Novel polypeptide-human ribosomal protein L3220.9 and encoding
PT   polynucleotide for treating diabetes, menstrual disorder, peptic ulcer,
PT   arrhythmia, anemia and epilepsy.
XX
PS   Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
XX
CC   The invention relates to the novel human ribosomal protein L3220.9, and
CC   the polynucleotide encoding it. The protein is useful for treating
CC   diabetes, menstrual disorder, peptic ulcer, arrhythmia, anaemia and
CC   epilepsy. Also disclosed is an antagonist for resisting the polypeptide
CC   and its therapeutic action, and the application of the polynucleotide.
CC   The present sequence encodes the human ribosomal protein L3220.9 of the
CC   invention
XX
SQ   Sequence 2591 BP; 576 A; 670 C; 557 G; 788 T; 0 U; 0 Other;

Query Match   11.3%; Score 359; DB 6; Length 2591;
Best Local Similarity   99.6%; Pred. No. 9.9e-162;
Matches   459; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1427 AGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTGTCCCCTGCTTTGAAACCATCG 1486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 AGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTGTCCCCTGCTTTGAAACCATCG 119

Qy   1487 CTGCCCTGGAGAATTACCACCCACGGCACTGGACTGAAGTGGCAGCTGGGACGGCATCTTTG 1546

Db   120 CTGCCCTGGAGAATTACCACCCACGGCACTGGACTGAAGTGGCAGCTGGGACGGCATCTTTG 179

Qy   1547 CACTCTTCCTGGGGGAACCTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTCA 1606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 CACTCTTCCTGGGGGAACCTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTCA 239

Qy   1607 AGCTTGCTAATGAAGAAGACAATAAAGAACACATCACTCACTGGAACTCTGTTTAACTATTACA 1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 AGCTTGCTAATGAAGAAGACAATAAAGAACACATCACTCACTGGAACTCTGTTTAACTATTACA 299

Qy   1667 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGACCCACCCCTGCACCCTGCGAGATGTGCCCC 1726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGACCCACCCCTGCACCCTGCGAGATGTGCCCC 359

Qy   1727 GGGGGTTCTTGCTGGGAGGACAGCTGTGGGCCATTGAATTCATGAGGCTGACGGTGCTGACA 1786
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 GGGGGTTCTTGCTGGGAGGACAGCTGTGGGCCATTGAATTCATGAGGCTGACGGTGCTGACA 419

Qy   1787 TGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGGCTTGTTTTTGTGCGGT 1846
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 TGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGGCTTGTTTTTGTGCGGT 479

Qy   1847 TCATGAACTACTGCTGTGTTGGTGCTGGGGACTTGGAGGCTGGATTT 1887
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   480 TCATGAACTACTGCTGTGTTGGTGCTGGGGACTTGGAGGCTGGATTT 520

RESULT 5
ADR07551
ID   ADR07551 standard; cDNA; 3566 BP.
XX
AC   ADR07551;
XX
DT   04-NOV-2004 (first entry)
XX
DE   Full length human cDNA useful for treating neurological disease Seq 1057.
XX
KW   gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
KW   osteoporosis; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; dementia; short memory; cancer;
KW   sense or motor function; emotional reaction; fear response; panic;
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   EP1447413-A2.
XX
PD   18-AUG-2004.
XX
PF   12-FEB-2004; 2004EP-00003145.
XX
PR   14-FEB-2003; 2003JP-00102207.
PR   09-MAY-2003; 2003JP-0013145Z.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's disease, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 1057; 2686pp; English.
XX

CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cytostatic and tranquiliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ Sequence 3566 BP; 989 A; 791 C; 877 G; 909 T; 0 U; 0 Other;

Query Match   9.7%; Score 308; DB 13; Length 3566;
Best Local Similarity   100.0%; Pred. No. 3.5e-137;
Matches 308; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1888 CCTTCATATGCTGAGTTTGATATTAGTGGAAAATGTGCTGGGTTTGATCTTCAACCAAGGA 1947
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   163 CCTTCATATGCTGAGTTTGATATTAGTGGAAAATGTGCTGGGTTTGATCTTCAACCAAGGA 222

Qy   1948 ATGATCTGGATGGGGCTCCTTCTATGCTCCAGGGCCTGGTGGGCATTAATGTGCTGCGCGCTG 2007
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   223 ATGATCTGGATGGGGCTCCTTCTATGCTCCAGGGCCTGGTGGGCATTAATGTGCTGCGCGCTG 282

Qy   2008 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGC 2067
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   283 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGC 342

Qy   2068 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCCTCCTGTCGTGGTGCTTC 2127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   343 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCCTCCTGTCGTGGTGCTTC 402

Qy   2128 CTCAGCCTCCTCGCGGTGGCCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGG 2187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 CTCAGCCTCCTCGCGGTGGCCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGG 462

Qy   2188 CCGTTCAG 2195
            ||||||||
Db   463 CCGTTCAG 470

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OM nucleic - nucleic search, using sw model

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description

No matches found

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OM nucleic - nucleic search, using sw model

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(without alignments)
10762.078 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgctgaccatgag..........atttctcaatccagaggaag 3169

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 110

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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10: /cgn2_6/ptcdata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3169	100.0	3169	9	US-10-792-307-3	Sequence 3, Appli
2	3074	97.0	3121	9	US-10-487-887-3	Sequence 3, Appli
3	1750	55.2	5027	9	US-10-450-763-28100	Sequence 28100, A
4	1648	52.0	4895	6	US-10-115-831-134	Sequence 134, App
5	493	15.6	2560	6	US-10-108-260A-342	Sequence 342, App
6	153	4.8	1060	5	US-10-027-632-122322	Sequence 122322,
7	153	4.8	1060	6	US-10-027-632-122322	Sequence 122322,

ALIGNMENTS

RESULT 1
US-10-792-307-3

; Sequence 3, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J.
; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227540
; CURRENT APPLICATION NUMBER: US/10/792,307
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 3169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-307-3

  Query Match   100.0%; Score 3169; DB 9; Length 3169;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 3169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 GTGAAAAGGCGGCGGGTGAAGACGCGGCGCTCTTCCACACAGGTGACACAGCTGGGAGGAGGATCC 120
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Db   61 GTGAAAAGGCGGCGGGTGAAGACGCGGCGCTCTTCCACACAGGTGACACAGCTGGGAGGAGGATCC 120

Qy   121 TCAAGCAAGCGGGCGCTCTCAAAGCCGAGGGGGGACCCCAGGCAGGCGGGAGCTCAGCGAAGC 180
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Qy   181 CAGAAGGAGGGGCCCCGGGGGGACCCCAAGCCCGGGGGTCTCCCCGGCGGGGGAAGCAAACAGGG 240
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Db   181 CAGAAGGAGGGGCCCCGGGGGGACCCCAAGCCCGGGGGTCTCCCCGGCGGGGGAAGCAAACAGGG 240

Qy   241 CCCAGAGAGACACAGAGAAGAGCTGGGGGACCAGCAGAGCGAGAGAGAGGACCTGC 300
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Db   301 GAGGGCAGGAGAGAAAGCCCGACGAGAGAGGGCCTCCTCCTTCCAGAGGCGGGAGCGCCCAAAG 360

Qy   361 AGGGAAAAGGAGGATTCCGAGGAAGGAAGGAGAGAAGTCGAAGCGGCGAGAAGAAACCCAGGTCA 420
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Db   361 AGGGAAAAGGAGGATTCCGAGGAAGGAAGGAGAGAAGTCGAAGCGGCGAGAAGAAACCCAGGTCA 420

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Qy   481 ATCCTGGACCAGGTGGAAGAAAAAAAAGAAGCTCATTGCCACCATGCCGAGGAGGCCCTGG 540
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Db   481 ATCCTGGACCAGGTGGAAGAAAAAAAAGAAGCTCATTGCCACCATGCCGAGGAGGCCCTGG 540

Qy   541 CCCATGGCGGAGAAGAACGTCGACACAGCTCAGGGAGGCCCAGGAGAATTTGTGGGAAGGTATGAA 600
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Db   541 CCCATGGCGGAGAAGAACGTCGACACAGCTCAGGGAGGCCCAGGAGAATTTGTGGGAAGGTATGAA 600

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Qy   661 AAATGGGTCAAATTTAAGAGAGACTTTGATAATTCAAGACTCAATGTATCCCTGGGAA 720
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Db   661 AAATGGGTCAAATTTAAGAGAGACTTTGATAATTCAAGACTCAATGTATCCCTGGGAA 720

Qy   721 ATGAAGATCAAGGACATTGAAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATCTTT 780
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Qy   781 CTCCGATGGATGTATGGGAGTTAAACCTTGTCCTTTTGGGCTTAATATTGGTCTAGTCATA 840
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Db   781 CTCCGATGGATGTATGGGAGTTAAACCTTGTCCTTTTGGGCTTAATATTGGTCTAGTCATA 840

Qy   841 ATCCCAGAGAGGTACTGATGGGCATGCCCTATGGGAGTTATTCCCAGAAAGACAGTGCCTCGG 900
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Db   901 GCTGAGGAGGAGAAAAGGCCATGGATTTTTCTTGTCCTTTGGATTTTGAGGGCTATATCAAG 960

Qy   961 TACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGACCATCGGGTGGCTGAGGTAC 1020
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Db   961 TACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGACCATCGGGTGGCTGAGGTAC 1020

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Db   1021 CGGCTGCCTATGGCTTACTTTATGGTGGGGGTCAGGGTGTCGGGCTACAGCCTGATTATT 1080

Qy   1081 GTCATTCGATCGATGGCCAGCAAATACCAAGGAACACAGGGGAGGGGAGAGTGACAAC 1140
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Db   1141 TTCACATTCAGCTTCAACAGTAGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACA 1200

Qy   1201 GCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACA 1260
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Qy  1441 ATGTCCCTGCTTGGAATGTTTCTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAAT 1500
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Db  1441 ATGTCCCTGCTTGGAATGTTTCTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAAT 1500

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Qy  1741 GAGACAGCTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACGCTGGTAACGTAC 1800
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Db  1741 GAGACAGCTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACGCTGGTAACGTAC 1800

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Db  1801 ATCACCATCCTGCTGCGGGGGACTTCCTACGGGCCTTGTTTGTTTTGTGCGGTTCATGAACTACTGC 1860

Qy  1861 TGGTGCTGGGGACTTGGAGGCTGGAATTTCCTTCATATGCTGAGTTTGATATTAGTGGAAAT 1920
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Db  1861 TGGTGCTGGGGACTTGGAGGCTGGAATTTCCTTCATATGCTGAGTTTGATATTAGTGGAAAT 1920

Qy  1921 GTCCTGGGTTTGATCTCAACCAAGGAAATGATCTGGATGGGCGTCCTCCTTCTATGCTCCAGGC 1980
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Db  1921 GTCCTGGGTTTGATCTCAACCAAGGAAATGATCTGGATGGGCGTCCTCCTTCTATGCTCCAGGC 1980

Qy  1981 CTGGTGGGGCATTAAATGTGCTGCGCCCTCGACCTCCATGTGACTTCCAGTGTGGGGCGTG 2040
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Qy  2041 ATGAGCAGCAAGCTACCCCATGAACGGGTGTTCAAAGCCTCCCGATCCAACACACTTCTAC 2100
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Qy  2281 GCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTACCTG 2340
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Db  2281 GCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTACCTG 2340

Qy  2341 AACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCACTGCCAGCTGAGAAGAAAATCCAAGTG 2400
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Qy  2401 CTCCGTGAAGTTGAGAAGAGTCACAAATCTGTAAAAGGGAAAGCCACACGACCAGAGATTCA 2460
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Qy  2461 GAGGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCCTCACCACTCACCAAGGAAGAG 2520
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Qy  2521 ACCACTCCTCCCTCTGCCAGCGCCAAAGCCAGCCCATGAGCAGAGGCCAGGGCCCTGGG 2580
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Qy  2581 ACCTCCAATTCTGCCAGCAGGACCACACTGCCTCGCCTCTGGACACCTCCTATATCTCGG 2640
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Db  2581 ACCTCCAATTCTGCCAGCAGGACCACACTGCCTCGCCTCTGGACACCTCCTATATCTCGG 2640

Qy  2641 CCCCTGGAATCGGACCAGAGATTCTGGCCACGCCACCCATCTCAGACTCATCCGTGGAGGTCA 2700
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Db  2641 CCCCTGGAATCGGACCAGAGATTCTGGCCACGCCACCCATCTCAGACTCATCCGTGGAGGTCA 2700

Qy  2701 GCCTCTGGAAAAGAGTGCTCAGAGACCTCCCACTACGGGTCTAGGGACTCCAGGGACCTCG 2760
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Db  2701 GCCTCTGGAAAAGAGTGCTCAGAGACCTCCCACTACGGGTCTAGGGACTCCAGGGACCTCG 2760

Qy  2761 ACCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAAAACCAAGGTTCTCTCCC 2820
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Db  2761 ACCCTAGGGCTGATCCTCAAGTACCCAGTTTCACACATACCAAAACCAAGGTTCTCTCCC 2820

Qy  2821 CTCTTTCCTCTCACATACATGCTCGTCTCTCTCCTTGGAATGCATGGAAGTCATTTGATTCCT 2880
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Qy  2881 TCAGGCCCTTGTCAGCTACCGAAGGAGGAAGAGCAGTGGCTTCACCTGTCCTTTAGGGAAG 2940
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Db  2881 TCAGGCCCTTGTCAGCTACCGAAGGAGGAAGAGCAGTGGCTTCACCTGTCCTTTAGGGAAG 2940

Qy  2941 CTGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGAGCTCTGAACC 3000
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Db   2941   CTGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGCTCGAACC   3000
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Qy   3001   CCACGCTCACAGTGGTCGACCTTGCCTCCCGATTTTCGGAGTTGGGGAAGGGGCCATGACC   3060
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Db   3001   CCACGCTCACAGTGGTCGACCTTGCCTCCCGATTTTCGGAGTTGGGGAAGGGGCCATGACC   3060

Qy   3061   ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGGTTTCTGCCAGCTTCCCT   3120
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Db   3061   ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGGTTTCTGCCAGCTTCCCT   3120

Qy   3121   AACCAGGAGGGGGATGGGAGAAGGGCCTACATTTCTCAATCCAGAGGAAG   3169
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RESULT 2
US-10-487-887-3

; Sequence 3, Application US/10487887
; Publication No. US20040249139A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
;   HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 3121
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-487-887-3

Query Match   97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity   100.0%; Pred. No. 0; Mismatches 0;
Matches 3074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   48   AGGTGACAGGCTGGGAAGGAGATCCTCAAGCCACGCGGGCTCTCAAAGCCCGAGGGGACCCC   107

Qy   156   AGGCAGGCGCGGGAGGCTCAGCGGAAGCCAAGAGGAGGCGCGCGGGGGGCCCAGCCCCGGG   215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108   AGGCAGGCGCGGGAGGCTCAGCGGAAGCCAAGAGGAGGCGCGCGGGGGGCCCAGCCCCGGG   167

Qy   216   GTCTCCCCGGAGGAAGCAAACAGGGGCCCAGGAGGACACAGAGGAGAGAGAGCTGGGGAGGA   275
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Db   168   GTCTCCCCGGAGGAAGCAAACAGGGGCCCAGGAGGACACAGAGGAGAGGGCCTCCTT   227

Qy   276   GGCGGGCGGCAGGCGAGGAGGCCGGAGGGCGGAGGAGGAAGCCCGAGGAGAGGGGCCTCCTT   335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228   GGCGGGCGGCAGGCGAGGAGGACCTGCGGAGTTGGGGAAGGGGCCATGACC   287

Qy   336   CCAGGAGCCGCAGCAGCGGCCCCAGAAGGGGAAAAGGGAGATTCCGAGGAGGAGGAGAAGTC   395
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Db   288   CCAGGAGCCGCAGCAGCCCCAGAAGGGGAAAAGGGAGATTCCGAGGAGGAGGAGAAGTC   347

Qy   396   GAAGGGGCAGAAGAGAAACCCAGGTCATCCTCCTTGGCCTCCAGTGCCTGCTTGGTGGGGAGTC   455
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Qy   456   CCTGTCCGAGGAGGAACTGGGCCCAGATCCTGGAGCAGGTGGAAGAAAAAGAAGCTCAT   515
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Qy   516   TGCCACCATGCGGAGCCAAGCCCTGGGCCATGGCGAAGCGAAGCAGGGAGGC   575
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Db   468   TGCCACCATGCGGAGCCAAGCCCTGGCCCATGGCGAAGCGAAGCTGACAGGAGGC   527

Qy   576   CCAGGAATTTGTGGAGAGTATGAAGGTGCCTTGGGAAAGGGGAAAGGCCAAGCACTATA   635
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Qy   636   TGCCTACAAGATGCTGATGGCCAAGAAATGGGTCAAATTTAAGAGAGACTTTGATAATTT   695
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Qy   696   CAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGACATTGAAAGTCACTTTGGTTC   755
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Db   648   CAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGACATTGAAAGTCACTTTGGTTC   707

Qy   756   TTCAGTGCCATGTATTCATCTTTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTT   815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   708   TTCAGTGCCATGTATTCATCTTTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTT   767

Qy   816   TGGCTTAATATTTGGTCTAGTCAATAATCCCAGAGGTACTACTGATGGGCCATGGGAG   875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   768   TGGCTTAATATTTGGTCTAGTCAATAATCCCAGAGGTACTACTGATGGGCCATGGGAG   827

Qy   876   TATTCCCAGAAAGACAGTGCCTCGGCTATATCAAGTACTACTGCTACTACAACAACCA   935
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828   TATTCCCAGAAAGACAGTGCCTCGGCTATATCAAGTACTACTGCTACTACAACAACCA   887

Qy   936   TTGGGATTTTGAGGCGCTATATATCAAGTACTCTGCACTCTTCATGGCTGGTCTACTACTA   995
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   888   TTGGGATTTTGAGGCGCTATATATCAAGTACTCTGCACTCTTCATGGCTGGTCTACTACTA   947

Qy   996   GAGAGACCATCGGGTGCTGGCTGAGGTACCGGCTGCCTATGGCTTTATGGTGGGGGGTCAG   1055
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   948   GAGAGACCATCGGGTGCTGGCTGAGGTACCGGCTGCCTATGGCTTTATGGTGGGGGGTCAG   1007

Qy   1056 CGTGTTCGGCTACAGCCTGATTATTGTCATTCGATCGATGGGCCAGCGCAATACCCAAGGAAG   1115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1008 CGTGTTCGGCTACACAGCCTGATTATTGTCATTCGATCGATGGGCCAGCGCAATACCCAAGGAAG   1067

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Qy  1116 CACAGGCGGAAGGGGGAGAGTGACAAACTTCACATTCAGCTTCAAAGATGTTCACCAGCTGGGA 1175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1068 CACAGGCGGAAGGGGGAGAGTGACAAACTTCACATTCAGCTTCAAAGATGTTCACCAGCTGGGA 1127

Qy  1176 CTACCTGATCGGGAAATTCAGAGACACGCTGATAAGCAACATTCACCACCAGCTT 1235
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1128 CTACCTGATCGGGAAATTCAGAGACACAGCTGATAAGCAAATATGCATCACCACCAGCTT 1187

Qy  1236 CAAGGAATCAATACTGGATGAACAAGAGAGTAACAAGAGAGAAAATATCATCTGACAAG 1295
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1188 CAAGGAATCAATACTGGATGAACAAGAGAGTAACAAGAGAGAAAATATCCATCTGACAAG 1247

Qy  1296 ATTTCTTCGTGTCTTGCCAACTTTCTCATCATCTGCTGTTTGTTGTGGGAGTGGGTACCT 1355
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1248 ATTTCTTCGTGTCTTGCCAACTTTCTCATCATCTGCTGTTTGTTGTGGGAGTGGGTACCT 1307

Qy  1356 CATTTACTTTGTGGTTAAGCGGATCTCAGCGAATTCTCCAAAATGCAGAAGTCAGCTGGTA 1415
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1308 CATTTACTTTGTGGTTAAGCGGATCTCAGCAATTCTCCAAAATGCAGAAGTCAGCTGGTA 1367

Qy  1416 TGAAAGGAAATGAGGTAGAGATCGTGATGTCCCTCCTTGGAATGTTTGTCCCCCTCTGTT 1475
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1368 TGAAAGGAAATGAGGTAGAGATCGTGATGTCCCTCCTTGGAATGTTTGTCCCCCTCTGTT 1427

Qy  1476 TGAAACCATGGCTGCCCTGGAGAATTACCACCACCGACTGAAGTGGCAGCTGGG 1535
         ||||||||||||||||||||||||||||||||||||||||||
Db  1428 TGAAACCATGGCTGCCCTGGAGAATTACCACCACCGACTGAAGTGGCAGCTGGG 1487

Qy  1536 ACCCATCTTTGCACTCTTCCTGGGGGAACCTCTACACATTTCTTCTTGGCCCTGATGGATGA 1595
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1488 ACCCATCTTTGCACTCTTCCTGGGGGAACCTCTACACATTTCTTCTTGGCCCTGATGGATGA 1547

Qy  1596 CGTCCACCTCAAGCTTGCTAATGAAGGACAATAAAGAAACTCACTCACTGGACTCTGTT 1655
         |||||||||||||||||||||||||||||||||||||||||||||
Db  1548 CGTCCACCTCAAGCTTGCTAATGAAGGACAATAAAGACACTCACTCACTGGACTCTGTT 1607

Qy  1656 TAACTATTACAACTCTTCTCGGTTGGAACGAGAGTGTCCCCGACCACCCTGACCCTGC 1715
         |||||||||||||||||||||||||||||||||||||||||||
Db  1608 TAACTATTACAACTCTTCTCGGTTGGAACGAGAGTGTCCCCGACCACCCTGACCCTGC 1667

Qy  1716 AGATGTGCCCCGCGGGGTTCTTGCTGCTGGGCATTGAATTCATTGAGGCTGAC 1775
         |||||||||||||||||||||||||||||||||||||||||||
Db  1668 AGATGTGCCCCGCGGGGTTCTTGCTGGGAGCAGTGTGGGCATTGAATTCATGAGGTGAC 1727

Qy  1776 GGTGCTGCTGACATGCTGGTAAGCTGTACATCACCATACATCTGTCTGTGGGGGACTTCCTACCGGGCTTG 1835
         |||||||||||||||||||||||||||||||||||||||||||
Db  1728 GGTGCTGCTGACATGCTGGTAAGCTGTACATCACCATACATCCTGGGGGACTTCCTACGGGGCTTG 1787

Qy  1836 TTTGTGCGGTTCATGAAACTACTGCTGCTGGGAGGCGTCGGATTTCCTTCATA 1895
         |||||||||||||||||||||||||||||||||||||||||||
Db  1788 TTTTGTGCGGTTCATGAAACTACTGCTGGGAGGCGTCGGATTTCCTTCATA 1847

Qy  1896 TGCTGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGAATGATCTG 1955
         |||||||||||||||||||||||||||||||||||||||||||
Db  1848 TGCTGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGAATGATCTG 1907
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Qy  1956 GATGGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAATTGTTGCGGCCTGCTGACCTC 2015
         |||||||||||||||||||||||||||||||||||||||||||
Db  1908 GATGGGGCTCCCTTCTATGCTCCAGGCCTGGTGGGCATTAATTGTTGCGGCCTGCTGACCTC 1967

Qy  2016 CATGTACTTCAGTGTCTGGGCGGGTGATGAGCAGCAGCGAACGTACCCCCATGAAGCGGTGTTCAA 2075
         |||||||||||||||||||||||||||||||||||||||||||
Db  1968 CATGTACTTCCAGTGTCTGGGCGGGTGATGAGCAGCAGCGAACGTACCCCATGAAGCGGTGTTCAA 2027

Qy  2076 AGCCTCCCGATCCAACAACTTCTACATGGGGCCTCCTGGTCGGTGGTTCCTTCCTCAGCCT 2135
         |||||||||||||||||||||||||||||||||||||||||||
Db  2028 AGCCTCCCGATCCAACAACTTCTACATGGGGCCTCCTGCTGCTGGTGGTTCCTTCCTCAGCCT 2087

Qy  2136 CCTGCGCGGTGGGCCTACACCATCATGTCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAG 2195
         |||||||||||||||||||||||||||||||||||||||||||
Db  2088 CCTGCCCGGTGGGCCTACACCATCATGTCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAG 2147

Qy  2196 TGGGAAAAACAGAAGTACGATGTCCTCCACAGAGACCATTGAAAACGAATTCCCAACTT 2255
         |||||||||||||||||||||||||||||||||||||||||||
Db  2148 TGGGAAAAACAGAAGTACGATGTCCTCCACAGAGACCATTGAAAACGAATTTCCCAACTT 2207

Qy  2256 CCTGGGGCAAGATCTTTGCTTTCCTCGCCAAATCCAGGCCTGATCATCCAGCCATCCTGCT 2315
         |||||||||||||||||||||||||||||||||||||||||||
Db  2208 CCTGGGGCAAGATCTTTGCTTTCCTCGCCAAATCCAGGCCTGATCATCCAGCCATCCTGCT 2267

Qy  2316 GATGTTCTTGGGCCATTTACTTACCTGAACTACAGTTTCCAAAAGCCTTTCCCGAGCTAATGC 2375
         |||||||||||||||||||||||||||||||||||||||||||
Db  2268 GATGTTCTTGGGCCATTTACTTACCTGAACTACAGTTTCCAAAAGCCTTTCCCGAGCTAATGC 2327

Qy  2376 CCAGCTGAGGGAAGAAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGATTCACAGATCTGTAAA 2435
         |||||||||||||||||||||||||||||||||||||||||||
Db  2328 CCAGCTGAGGGAAGAAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGATTCACAGATCTGTAAA 2387

Qy  2436 AGGCAAAAGCCACAGCCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAATGCCAC 2495
         |||||||||||||||||||||||||||||||||||||||||||
Db  2388 AGGCAAAAGCCACAGCCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAATGCCAC 2447

Qy  2496 CCAGCTCCAACTCACCAAGGAAGAGACCACTCCTCCCTCTGCCAGCCAAAAGCCAGGCCAT 2555
         |||||||||||||||||||||||||||||||||||||||||||
Db  2448 CCAGCTCCAACTCACCAAGGAAGAGACCACTCCTCCCTCTGCCAGCCAAAAGCCAGGCCAT 2507

Qy  2556 GGACAAGAGACGGGCGGCAGGGCCCTGGGGACCTCCAATTCTCGCCAGCAGGACCACACTGCCTGC 2615
         |||||||||||||||||||||||||||||||||||||||||||
Db  2508 GGACAAGAGACGGGCGGCAGGGCCCTGGGGACCTCCAATTCTCGCCAGCAGGACCACACTGCCTGC 2567

Qy  2616 CTCTGGACAACCTTCCTATATCTCGGCCCCCCTGGAATCGGACCAGATTCTTGGCCAGCCCCC 2675
         |||||||||||||||||||||||||||||||||||||||||||
Db  2568 CTCTGGACAACCTTCCTATATCTCGGCCCCCTGGAATCGGACCAGATTCTTGGCCAGCCCCC 2627

Qy  2676 ATCTCAGACTCATCCGCTGGAGGTCAGCCCTCTGGAAAGAGTGCTCAGAGACTGCCCACTG 2735
         |||||||||||||||||||||||||||||||||||||||||||
Db  2628 ATCTCAGACTCATCCGTGGAGGTCAGCCTCTGGAAAGAGTGCTCAGAGACTGCCCACTG 2687

Qy  2736 ACGGCTAGGACTCCAGGGAGGCCTCGACCCTGAGCCTGATCGTCAAGTACCCCAGTTTCAC 2795
         |||||||||||||||||||||||||||||||||||||||||||
Db  2688 ACGGCTAGGACTCCAGGGAGGCCTCGACCCTAGGGCTGATCCTCAAGTACCCCAGTTTCAC 2747

Qy  2796 ACATACCAAAACCAAGGTTCTCTCCCCTCTTCCTCTCACATACATGCTTCTGTGTCCTCTC 2855
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RESULT 3

Query Match   55.2%; Score 1750; DB 9; Length 5027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   947 AGGGCTATATCAAGTACTCTGCACTCTCTATGGCTACTCATCACAAACAACCAGAGAGACCATCG 1006
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1094 AGGGCTATATCAAGTACTCTGCACTCTCTATGGCTACTCATCACAAACAACCAGAGAGACCATCG 1153

Qy 1007 GGTGGCCTGAGGTACCGGCTACCTGCCTATGGCTTACTTTTATGGTGGGGGGTCAGCGTGTTCGGCT 1066
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1154 GGTGGCCTGAGGTACCGGCTACCTGCCTATGGCTTACTTTTATGGTGGGGGGTCAGCGTGTTCGGCT 1213

Qy 1067 ACAGCCTGATTATTGTCATTCGATGCGATGGCCAGCAAATACCCAAGGAAGACACAGGCGGAG 1126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1214 ACAGCCTGATTATTGTCATTCGATGCGATGGCCAGCAAATACCCAAGGAAGACACAGGCGGAG 1273

Qy 1127 GGGAGAGTGACAAACTTCACATTCACGCTTCACAGATGTTCACCAGCTGGGACTACCTGATCG 1186
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1274 GGGAGAGTGACAAACTTCACATTCACGCTTCACAGATGTTCACCAGCTGGGACTACCTGATCG 1333

Qy 1187 GGAATTCAGAGACACGCTGATTAACAAAATAATGCATCCATCACCAGAGCTTCAAGGAATCAA 1246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1334 GGAATTCAGAGACACGCTGATTAACAAAATAATGCATCCATCACCAGAGCTTCAAGGAATCAA 1393

Qy 1247 TAGTGGATGAACAGAGAGTAACAAAGAAGAAAAATATCCATCTGACAGAGATTTCTTCGTG 1306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1394 TAGTGGATGAACAGAGAGTAACAAAGAAGAAAAATATCCATCTGACAGAGATTTCTTCGTG 1453

Qy 1307 TCCTGGCCAACTTCTCATCATCACTCTGTTTGTTGTGGAAGTGGGTACCTCATTTACTTTG 1366
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1454 TCCTGGCCAACTTCTCATCATCACTCTGTTTGTTGTGGAAGTGGGTACCTCATTTACTTTG 1513

Qy 1367 TGGTTAACGGATCTCAGCAAATTCTCCAAAATGCAGAANTGCAGAANTGTCAGCTGGTATGAAAGGAATG 1426
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1514 TGGTTAACGGATCTCAGCAAATTCTCCAAAATGCAGAANTGTCAGCTGGTATGAAAGGAATG 1573

Qy 1427 AGGTAAGGAGTCGTGATGTCCCTGCTTGGAAGTGTTTTGTCCCCCTCTGTTTGAAACCACG 1486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1574 AGGTAGAGATCGTGATGTCCCTGCTTGGAAGTGTTTTGTCCCCCTCTGTTTGAAACCATCG 1633

Qy 1487 CTGCCCTGGAGAATTACCACCCACGCCACTGGACTGAAAGTGGCCAGCGTGGGACCCATCTTTG 1546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1634 CTGCCCTGGAGAATTACCACCCACGCCACTGGACTGAAAGTGGCCAGCGTGGGACCCATCTTTG 1693

Qy 1547 CACTGCTTCCTGGGGAACCTCACACATTTCTCTTGGCCCTGATGATGACGTCACCTCA 1606
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1694 CACTGCTTCCTGGGGAACCTCACACATTTCTCTTGGCCCTGATGATGACGTCCACCTCA 1753

Qy 1607 AGCTTGCTAATGAAGGAGACAATAAAGAACATCACTGGACTCTGTTAACTATTACA 1666
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1754 AGCTTGCTAATGAAGGAGACAATAAAGAACATCACTGGACTCTGTTAACTATTACA 1813

Qy 1667 ACTCTTCTGGTTGGAACGAGAGAGTGTCCCCGACACCCTGCACCCTGCAGATGCCCC 1726
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1814 ACTCTTCTGGTTGGAACGAGAGAGTGTCCCCGACACCCTGCACCCTGCAGATGCCCC 1873

Qy 1727 GGGGGTTCTTGCTGTGGGAGGACAGCTGTGGGCATTGAATTCATGAGGGTGACGGGTGTCTGACA 1786

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Db  1874  GGGGTTCTTGCTGGGAGGACGACGCTGTGGGCATTGAATTCATGAGGCGTGACGGGTGTCTGACA
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy  1787  TGCTGGTAAGGTACATCACCATCCTGCTGGGGGACTTCCTACGGGGTTGTTTTGTGCGGGT  1846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1934  TGCTGGTAAGGTACATCACCATCCTGCTGGGGGACTTCCTACGGGGCTTGTTTTGTGCGGGT  1993

Qy  1847  TCATGAACTACTCGTCGTGGTGCTGGGGACTTGAGGCTTGAATTTCTTCATTATGTCTGAGTTTG  1906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1994  TCATGAACTACTCGTCGTGGTGCTGGGGACTTGAGGCTTGAATTTCTTCATTATGTCTGAGTTTG  2053

Qy  1907  ATATTAGTTGGAAAATGTGCTGGGTTTGATCTTCACCAAGGAATGGATGGGCTCCT  1966
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2054  ATATTAGTTGGAAAATGTGCTGGGTTTGATCTTCACCAAGGAATGATCTGGATGGGCTCCT  2113

Qy  1967  TCTATGCTCCAGGGCCTGGTGGGGCATTAATGTGCTGGCGCCTGCTGACCTCCATGTACTTCC  2026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2114  TCTATGCTCCAGGGCCTGGTGGGGCATTAATGTGCTGGCTGACCTCCATGTACTTCC  2173

Qy  2027  AGTGCTGGGCGGGTGATGAGGAGCAAGTTACCCGATGAGGCGTGTTCAAAGCCTTCCGAT  2086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2174  AGTGCTGGGCGGGTGATGAGGAGCAAGTTACCCGATGAGGCGTGTTCAAAGCCTCCCGAT  2233

Qy  2087  CCAACAACTTCTCACATGGGGCCTCCTGCTGCTGGTGTCTTCTTCCTCAGCCTCCTGCCGGTGG  2146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2234  CCAACAACTTCTCACATGGGGCCTCCTGCTGCTGGTGTCTTCCTCCTCAGCCTCCTGCCGGTGG  2293

Qy  2147  CCTACACCATCATGTCCCTCCCTCCTTTGACTGCGGGGCCGTTCAGTGGGGAAAAACA  2206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2294  CCTACACCATCATGTCCCTCCCACCTCCTTTGACTGCGGGGCCGTTCAGTGGGGAAAAACA  2353

Qy  2207  GAATGTACGATGTCCTCCAAGAGACCATTGAAAAACGATTTCCCAAACTTCCTGGGCAAGA  2266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2354  GAATGTACGATGTCCTCCAAGAGACCATTGAAAAACGATTTCCCAAACTTCCTGGGCAAGA  2413

Qy  2267  TCTTTGCTTTCCTCGCCAATCCAGGGCTGATCATCCCAGCCATCCTGCTGATGTTCTTGG  2326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2414  TCTTTGCTTTCCTCGCCAATCCAGGGCTGATCATCCCAGCCATCCTGCTGATGTTCTTGG  2473

Qy  2327  CCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGA  2386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2474  CCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGA  2533

Qy  2387  AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGTCACAAATCTGTAAAAGGAAAAGCCA  2446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2534  AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGTCACAAATCTGTAAAAGGAAAAGCCA  2593

Qy  2447  CAGCCAGAGATTCAGGAGGACACACCTCCAAAAATGCCACCCAGCTCCAAC  2506
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2594  CAGCCAGAGATTCAGGAGGACACACCTCCAAAAATGCCACCCAGCTCCAAC  2653

Qy  2507  TCACCAAGGAAGAGAGAGCACCACTCCTCCCTCTGCCACCCAAAGCCAGGCCCATGGACAAGAAGG  2566
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2654  TCACCAAGGAAGAGAGACCACTCCTCCCTCTGCCACCCAAAGCCAGGCCCATGGACAAGAAGG  2713

Qy  2567  CGCAGGGCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGCCTCTGGACACC  2626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2714  CGCAGGGCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGCCTCTGGACACC  2773

Qy  2627  TTCCTATATCTCGGGCCCCCTGGAATCGGACCAGAGATTCTGGGCCAGCGCCCCAATCTCAGACTC  2686
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2774  TTCCTATATCTCGGGCCCCCTGGAATCGGACCAGAGATTCTGGGCACCGGCCCCAATCTCAGACTC  2833

Qy  2687  ATCCGTGGAG  2696
          ||||||||||
Db  2834  ATCCGTGGAG  2843
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Query Match        52.0%;   Score 1648;   DB 6;   Length 4895;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 1748;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   947  AGGGCTATATCAAGTACTCTGGACTCTTCTATGGCTACTACAACAACCAGAGGACCCATCG  1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1094  AGGGCTATATCAAGTACTCTGGACTCTTCTATGGCTACTACAACAACCAGAGGACCCATCG  1153

Qy  1007  GGTGGCTGAGGTACCGGCGTGCCTATGGCTTACTTTATGGTGGGGGTTCACGCGTGTCGGGCT  1066
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1154  GGTGGCTGAGGTACCGGCTGCCTATGGCTTACTTTATGGTGGGGGTTCACGCGTGTTCGGGCT  1213

Qy  1067  ACAGCCTGATTATTGTCATTCGATCGATGGCCGCAATACCCAAGGAAGCCACAGGCCGGAAG  1126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1214  ACAGCCTGATTATTGTCATTCGATCGATGGCCGCAAATACCCAAGGAAGCCACAGGCCGGAAG  1273
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Qy   1127 GGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCACTGGACTACCTGATCG 1186
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1274 GGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCACTGGACTACCTGATCG 1333

Qy   1187 GGAATTCAGAGACAGCAGCTGATAACAAAATAATGCATCCATCACCACCACCAGCTTCAAGGAATCA 1246
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1334 GGAATTCAGAGACAGCAGCTGATAACAAAATAATGCATCCATCACCACCACCAGCTTCAAGGAATCA 1393

Qy   1247 TAGTGGATGAACAAGAGAGTAACAAAGAGAGAGAAAATAATCCATCTGACAAGATTTCTTCGGTG 1306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1394 TAGTGGATGAACAAGAGAGTAACAAAGAGAGAGAAAATAATCCATCTGACAAGATTTCTTCGGTG 1453

Qy   1307 TCCTGGCCAACTTCATCTGCTGCTTGTTTGTGTTGGAAGTGGGTACCTCATTACTTTG 1366
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1454 TCCTGGCCAACTTCATCTGCTGCTTGTTTGTGTTGGAAGTGGGTACCTCATTACTTTG 1513

Qy   1367 TGGTTAAGGCGATCTCAGCAATTCTCCAAAATGCAGAAATGTCACCTGGTATGAAAGGAAATG 1426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1514 TGGTTAAGGCGATCTCAGCAATTCTCCAAAATGCAGAAATGTCACCTGGTATGAAAGGAAATG 1573

Qy   1427 AGGTAGAGAATCGTGATGTCCCTGCTTGGAAATGTTTTGTCCCCCTCTGTTTGAAACCATCG 1486
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1574 AGGTAGAGAATCGTGATGTCCCTGCTTGGAAATGTTTTGTCCCCCTCTGTTTGAAACCATCG 1633

Qy   1487 CTGCCCTGGAGAATTACCACCCAGCCATGGACTGAAGTGGCAGCCTGGGACGACGCATCTTTG 1546
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1634 CTGCCCTGGAGAATTACCACCCAGCCATGGACTGAAGTGGCAGCCTGGGACGACGCATCTTTG 1693

Qy   1547 CACTCTTCCTGGGGGAACCTCTACACATTTCTTCTTGTGCCCTGATGGATGACGTCCACCTCA 1606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1694 CACTCTTCCTGGGGGAACCTCTACACATTTCTTCTTGTGCCCTGATGGATGACGTCCACCTCA 1753

Qy   1607 AGCTTGCTAATGAAGACAATAAAGACATCACTCACTGGACTCTCTGTTTAACTATTACA 1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1754 AGCTTGCTAATGAAGACAATAAAGACATCACTCACTGGACTCTCTGTTTAACTATTACA 1813

Qy   1667 ACTCTTCTGGTTGGAACGGAGTGTCCCCGACCACCCCTGCACCCTGCAGATGTGCCCC 1726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1814 ACTCTTCTGGTTGGAACGGAGTGTCCCCGACCACCCCTGCACCCTGCAGATGTGCCCC 1873

Qy   1727 GGGGTTCTTGCTGCTGGAGACAGCGTGTGGGCATTGAATTCATGAGGGTGACGGGTGTCTGACA 1786
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1874 GGGGTTCTTGCTGCTGGAGACAGCGTGTGGGCATTGAATTCATGAGGGTGACGGGTGTCTGACA 1933

Qy   1787 TGCTGGTAAGCGTACATCACCATCCTGCTCGGGGGACTTCCTCACGGGCTTGTTTTTGTCGGGT 1846
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1934 TGCTGGTAAGCGTACATCACCATCCTGCTCGGGGGACTTCCTCACGGGCTTGTTTTTGTCGGGT 1993

Qy   1847 TCATGAACTACTGCTGGTGCTGGGAGACTTGGAGGCTGGATTTCCTTCATATGCTGAGTTTG 1906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1994 TCATGAACTACTGCTGGTGCTGGGAGACTTGGAGGCTGGATTTCCTTCATATGCTGAGTTTG 2053

Qy   1907 ATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCT 1966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2054 ATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCT 2113

Qy   1967 TCTATGCTCCAGGCCCTGGTGGGCCATTAATGTGCTGGGCCTGCTGTGACCTCCATGTACTTCC 2026
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2114 TCTATGCTCCAGGCCCTGGTGGGCCATTAATGTGCTGGGCCTGCTGTGACCTCCATGTACTTCC 2173

Qy   2027 AGTGCTGGGCGGGTGATGAGCAGCAAGTACCCCGATGACGAACGGCGTGTTCAAAGCTCCCGAT 2086
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2174 AGTGCTGGGCGGGTGATGAGCAGCAAGTACCCCGATGACGAACGGCGTGTTCAAAGCTCCCGAT 2233

Qy   2087 CCAACAACTTCTACATGGGGCCTCCTGCTGCTGGGTGCTCTTCCTCAGCCTCCTGCCGGGTGG 2146
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2234 CCAACAACTTCTACATGGGGCCTCCTGCTGCTGGGTGCTCTTCCTCAGCCTCCTGCCGGGTGG 2293

Qy   2147 CCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGCGGCCGGTTCAGTGGGGAAAAACA 2206
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2294 CCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGCGGCCGGTTCAGTGGGGAAAAACA 2353

Qy   2207 GAATGTACGGATGTCCTCCAAGAGACACCATTGAAAAACGAATTCCCAAACTTCCTGGGCAAGA 2266
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2354 GAATGTACGGATGTCCTCCAAGAGACACCATTGAAAAACGAATTCCCAAACTTCCTGGGCAAGA 2413

Qy   2267 TCTTTGCTTTTCCTCGGCAAATCCAGGCCTGATCATCCCAGCCATCTGCTGATGTTCTTGG 2326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2414 TCTTTGCTTTTCCTCGGCAAATCCAGGCCTGATCATCCCAGCCATCTGCTGATGTTCTTGG 2473

Qy   2327 CCATTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGA 2386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2474 CCATTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGA 2533

Qy   2387 AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGGTCACAAATCTGTAAAGGCAAAGCCA 2446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2534 AGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGGTCACAAATCTGTAAAGGCAAAGCCA 2593

Qy   2447 CAGCCAGAGATTCAGAGGACACACTAAAAGCAGCTCCAAAAATGCCACCAGCTCCAAC 2506
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2594 CAGCCAGAGATTCAGAGGACACACTAAAAGCAGCTCCAAAAATGCCACCAGCTCCAAC 2653

Qy   2507 TCACCAAGGAAGAGACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGG 2566
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2654 TCACCAAGGAAGAGACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGG 2713

Qy   2567 CGCAGGGGCCCTGGGACCTCCAAATCTGCCAGCAGCACACACTGCCTGCCTCTGGACACC 2626
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2714 CGCAGGGGCCCTGGGACCTCCAAATCTGCCAGCAGCACACACTGCCTGCCTCTGGACACC 2773

Qy   2627 TTCCTATATCTCGGCCCCCCTGGAATCGGACACGGGCACGCGCCCCATCTCAGACTC 2686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2774 TTCCTATATCTCGGCCCCCCTGGAATCGGACACAGAGATTCTTGGCCGCCCCACCCCCATCTCAGACTC 2833

Qy   2687 ATCCGTGGAG 2696
          ||||||||||
Db   2834 ATCCGTGGAG 2843

RESULT 5
US-10-108-260A-342
; Sequence 342, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US2004000560Ale1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 342
; LENGTH: 2560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-342

Query Match   15.6%;   Score 493; DB 6; Length 2560;
Best Local Similarity 99.7%;   Pred. No. 1.2e-252;
Matches 593; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1293 AAGATTTCTTCGTTCGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTTGTGTGGAAGTGGGTA 1352
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 AAGATTTCTTCGTTCGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTTGTGTGGAAGTGGGTA 60

Qy   1353 CCTCATTTACTTTGTGGTTAAGCGGATCTCAGCAATTCTCCAAAATGCAGAATGTCAGCTG 1412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CCTCATTTACTTTGTGGTTAAGCGGATCTCAGCAATTCTCCAAAATGCAGAATGTCAGCTG 120

Qy   1413 GTATGAAAGGAATGAGGTAGAGATCCGTGATGTCCCTGCTTGGGAATGTTTTGTCCCCTCT 1472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GTATGAAAGGAATGAGGTAGAGATCCGTGATGTCCCTGCTTGGGAATGTTTTGTCCCCTCT 180

Qy   1473 GTTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACCGGACTGAAGTGGGCAGCT 1532
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACCGGACTGAAGTGGGCAGCT 240

Qy   1533 GGGACGCGCATCTTTGCACTCTTCCTGGGGGAACCTCACACATTTCTTCTCTGGCCCTGATGGA 1592
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GGGACGCGCATCTTTGCACTCTTCCTGGGGGAACCCTCACACATTTCTTCTCTGGCCCTGATGGA 300

Qy   1593 TGACGTCCACCTCAAGCGTTGCTAATGAAGAGAACAAATAAAAGAAACATCACTCACTGGACTCT 1652
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGATGTCCACCTCAAGCGTTGCTAATGAAGAGAACAAATAAAAGAAACATCACTCACTGGACTCT 360

Qy   1653 GTTTAACTATTACAACTCTTCTCGGTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCC 1712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTTAACTATTACAACTCTTCTCGGTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCC 420

Qy   1713 TGCAGATGTGCCCCGGGGTTCTTCTTGCTGGGAGACAGCTGTGGGGCATTGAATTCATGAGGCT 1772
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGCAGATGTGCCCCGGGGTTCTTGCTGCTGGGAGACAGCTGTGGGGCATTGAATTCATGAGGCT 480

Qy   1773 GACGGTGTCTGCATGCTGGTAAGGTACATCACCATCCTCGCTGGGGGACTTCCTACGGGGC 1832
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GACGGTGTCCGACATGCTGGTAAGGTACATCACCATCCTCGCTGGGGGACTTCCTACGGGGC 540

Qy   1833 TTGTTTTGTGCGGTTCATGAACTACTGCGTCGGTCGCTGGGACTTGGAGGCTGGATTT 1887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTGTTTTGTGCGGTTCATGAACTACTGCGTCGGTCGCTGCTGGGACTTGGAGGCTGGATTT 595

RESULT 6
US-10-027-632-122322/c
; Sequence 122322, Application US/10027632
; Publication No. US2002019371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SEQ ID NO 122322
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122322

Query Match   4.8%;   Score 153; DB 5; Length 1060;
Best Local Similarity 100.0%;   Pred. No. 2e-70;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1607 AGCTTGCTAATGAAGAGAACAATAAAAGAACATCACTCACTGGACTCTGTTTAACTATTACA 1666
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 AGCTTGCTAATGAAGAGAACAATAAAAGAACATCACTCACTGGACTCTGTTTAACTATTACA 612

Qy   1667 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCCTGCACCGATGTGCCCC 1726
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGACCACCCCTGCACCCTGCAGATGTGCCCC 552

Qy   1727 GGGGTTCTTCTTGCTGGGGAGACAGCGTGTGGGCATTG 1759
          ||||||||||||||||||||||||||||||||||||
Db   551 GGGGTTCTTGCTGCTGGGAGACAGCGTGTGGGCATTG 519

RESULT 7
US-10-027-632-122322/c
; Sequence 122322, Application US/10027632
; Publication No. US2003020407SA9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 122322
LENGTH: 1060
TYPE: DNA
ORGANISM: Human
US-10-027-632-122322

Query Match   4.8%; Score 153; DB 6; Length 1060;
Best Local Similarity   100.0%; Pred. No. 2e-70;
Matches 153; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1607 AGCTTGCTAATGAAGAGACAATAAAAGAAACATCACTCACTGGGACTCTGTTTAACTATTACA 1666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 AGCTTGCTAATGAAGAGACAATAAAAGAAACATCACTCACTGGGACTCTGTTTAACTATTACA 612

Qy   1667 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGCACCACCCCTGCACCCTGCAGATGTGCCCC 1726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 ACTCTTCTGGTTGGAACGAGAGTGTCCCCGCACCACCCCTGCACCCTGCAGATGTGCCCC 552

Qy   1727 GGGGTTCTTGCTGCTGGGAGACGAGCAGCTGTGGGCATTG 1759
             ||||||||||||||||||||||||||||||||||||
Db   551 GGGGTTCTTGCTGCTGGGAGACGAGCAGCTGTGGGCATTG 519

Search completed: December 6, 2005, 04:45:10
Job time : 2438 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:06 ; Search time 499 Seconds
                   (without alignments)
                   1976.466 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgctgaccatgag..........atttctcaatccagaggag 3169

Scoring table: OLIGO_NUC
                   Gapop 60.0 , Gapext 60.0

Searched: 3289935 seqs, 155610033 residues

Word size :   110

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published Applications_NA_New:*
           1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
           2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
           3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
           4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
           5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
           6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
           7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
           8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
           9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
          10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   Query
No.   Score   Match Length DB   ID   Description

No matches found

Search completed: December 6, 2005, 04:04:22
Job time : 499 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 12:30:01 ; Search time 12014 Seconds
                                              (without alignments)
                                              12341.291 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgaccatgag.............attctcaatccagoaggaag 3169

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339541228 residues

Word size :   110

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	DB	Description
1	308	9.7	1827	10	AY406224	AY406224 Homo sapi
2	241	7.6	247	6	CD635963	CD635963 56089332H
c	3	241	7.6	247	6	CD635964	CD635964 56089332J

ALIGNMENTS

RESULT 1
AY406224
LOCUS   AY406224   1827 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION   Homo sapiens TMC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
                genomic survey sequence.
ACCESSION   AY406224
VERSION   AY406224.1   GI:39762198
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE   1 (bases 1 to 1827)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
                gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 1827)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
                them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1827
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1..>1827
                     /gene="TMC2"
                     /locus_tag="HCM2486"
ORIGIN

Query Match   9.7%; Score 308; DB 10; Length 1827;
Best Local Similarity   100.0%; Pred. No. 4e-148;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1888 CCTTCATATGCTGAGTTTGATATTAGTGGAAATGYGCTGGGTTTGATCTTCAACCAAGGA 1947
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   979 CCTTCATATGCTGAGTTTGATATTAGTGGAAATGYGCTGGGTTTGATCTTCAACCAAGGA 1038

Qy   1948 ATGATCTGGATGAGGCCTCCTTCTTCTATGCTCCAGCCCTGGTGGGCATTAATGTGCTGCCCTG 2007
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 ATGATCTGGATGGGCCTCCTTCTTCTATGCTCCAGCCCTGGTGGGCATTAATGTGCTGCCCTG 1098

Qy   2008 CTGACCTCCATGTACTTCCAGTGCTGGGCGGGTGATGAGCGAAGCGTACCCCATGAAGGC 2067
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RESULT 2
CD635963
LOCUS   CD635963   247 bp   mRNA   linear   EST 12-JAN-2004
DEFINITION 560893321H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD635963
VERSION   CD635963.1 GI:40284230
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
  PUBMED   15203218
COMMENT   Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 650845102
            Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
     source   1..247
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match   7.6%; Score 241; DB 6; Length 247;
Best Local Similarity   100.0%; Pred. No. 3e-113;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   67 CAAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCAGCTGATAACAAATA 126

Qy 1215 TGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAAGAGTAACAAGA 1274
Db 127 TGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAAGAGTAACAAGA 186

Qy 1275 AGAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTG 1334
Db 187 AGAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTG 246

Qy 1335 T 1335
Db 247 T 247

RESULT 3
CD635964/c
LOCUS   CD635964   247 bp   mRNA   linear   EST 12-JAN-2004
DEFINITION 560893322I1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD635964
VERSION   CD635964.1 GI:40284231
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
  PUBMED   15203218
COMMENT   Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 650845102
            Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
     source   1..247
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

Query Match   7.6%; Score 241; DB 6; Length 247;
Best Local Similarity   100.0%; Pred. No. 3e-113;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 CAAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATAACAAATA 122

Qy 1215 TGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAGAGTAACAAAGA 1274
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TGCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAGAGTAACAAAGA 62

Qy 1275 AGAAAATAATCCATCTGACAAAGATTTCTTCGGTGTCCTGGGCCAACTTTCTCATCATCTGCTG 1334
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61   AGAAAATAATCCATCTGACAAAGATTTCTTCGGTGTCCTGGGCCAACTTTCTCATCATCTGCTG 2

Qy 1335 T 1335
         |
Db 1   T 1

Search completed: December 5, 2005, 23:34:52
Job time : 12015 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 03:45:30 ; Search time 15410 Seconds
                   (without alignments)
                   11689.610 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgctgaccatgag.........atttctcaatccagaggaag 3169

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172565 3 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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     c 9: gb_ro:*
     c 10: gb_sts:*
        11: gb_sy:*
        12: gb_un:*
        13: gb_vi:*
        14: gb_htg:*
        15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   Query   Match
No.   Score   %   Length DB   ID   Description
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  1   3169   100.0   3169   8 AF417580   AF417580 Homo sapi
  2   1957.6 61.8   3216   9 AF417581   AF417581 Mus muscu

ORGANISM Homo sapiens
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          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE   1 (bases 1 to 3169)
  AUTHORS   Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
            Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
            Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Riazuddin,S.,
            Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F.,
            Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
  TITLE   Dominant and recessive deafness caused by mutations of a novel
            gene, TMC1, required for cochlear hair-cell function
  JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
   PUBMED   11850618
REFERENCE   2 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
REFERENCE   3 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
  REMARK   Sequence update by submitter
COMMENT   On Mar 3, 2003 this sequence version replaced gi:19223982.
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Search completed: November 30, 2005, 09:34:05
Job time : 15427 secs

OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 01:28:55 ; Search time 1704 Seconds
                                             (without alignments)
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Perfect score: 3169
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Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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SUMMARIES

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3	1957.6	61.8	3216 8 ACC69616	Acc69616 Mouse tra
4	816.8	25.8	2895 8 ACC69615	Acc69615 Mouse tra

5	814.2	25.7	4333	8	ACC69613	Acc69613 Human tra
6	591.8	18.7	2560	11	ADM01657	Adm01657 Human cDN
7	463.4	14.6	2591	6	ABV75613	Abv75613 Human rib
8	437.6	13.8	3357	13	ADU01837	Adu01837 Novel hum
9	356.4	11.2	3897	13	ADU01668	Adu01668 Novel hum
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ALIGNMENTS

RESULT 1

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ACC69614
ID   ACC69614 standard; cDNA; 3121 BP.
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AC   ACC69614;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Human transductin-2 (TDC2) encoding cDNA SEQ ID NO:3.
XX
KW   Human; transduction-2; TDC2; hearing loss; auditory; gene therapy; gene;
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KW   ss.
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OS   Homo sapiens.
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FH   Key             Location/Qualifiers
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PD   27-MAR-2003.
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PF   19-SEP-2002; 2002WO-US029614.
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PR   19-SEP-2001; 2001US-0323275P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Griffith AJ, Kurima K, Wilcox E, Friedman T;
XX
DR   WPI; 2003-371806/35.
DR   P-PSDB; ABR43616.
XX
PT   An isolated or purified nucleic acid molecule encoding transductin-1
PT   (TDC1), TDC2, or its fragment, useful for prognosticating, treating or
PT   monitoring hearing loss.
XX
PS   Claim 9; Fig 2; 85pp; English.
XX
CC   The present sequence encodes human transductin-2 (TDC2). The present
CC   invention describes human and mouse TDC1 and TDC2. Also described: (1) a
CC   method for detecting hearing loss or predisposition to hearing loss in an
CC   animal; (2) a method for determining the level of nucleic acid comprising
CC   wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
CC   sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
CC   gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
CC   method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
CC   TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
CC   type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
CC   comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
CC   and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
CC   for treating an animal prophylactically or therapeutically for hearing
CC   loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
CC   a method for identifying one or more agents that interact with a TDC1
CC   and/or TDC2 genes in a cell by administering one or more agents to the
CC   cell comprising the genes and assaying the expression level of the genes
CC   by the cell, where an increase or decrease in the expression level is
CC   indicative of the interaction between the agents and the genes in the
CC   cell. TDC1 and TDC2 have auditory activities and can be used in gene
CC   therapy. The molecules, compositions and methods of the present invention
CC   can be used for prognosticating, treating and monitoring hearing loss
XX
SQ   Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;
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Query Match   97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity   100.0%; Pred. No. 0;

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Matches 3074;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    96 AGGTGACAGGCTGGGAAGGAGGAATCCTCAAGCCAAGCCGGCTTCTCAAAGCCGAGGGGACCCC 155
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Db    48 AGGTGACAGGCTGGGAAGGAGGAATCCTCAAGCCAAGCCGGCTTCTCAAAGCCGAGGGGACCCC 107

Qy   156 AGGCAGGCGGCGGGAGACTCAGCGAAGCAGGACCAGAAGAGACCGCCGCCCGGGGGGCACCCCAGCCCCGG 215
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Db   108 AGGCAGGCGGCGGGAGCTCAGCGAAGCAGGAAGAGACCGCCGCCCGGGGGGCCCAACCCCGGG 167

Qy   216 GTCTCCCCGCGGAGGAAGCAGAGGAGACGCACAGAGAGAGCTGGGGAGCAGGA 275
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   168 GTCTCCCCGCGGAGGAAGCAAACAGGGGCGCCCAGGAGACACAGAGAGAGCTGGGGAGCAGGA 227

Qy   276 GCCGGGCGGAGGCCAGAGGACCTGCAGGGCCAGGAGACGGGAAAACGCGGCCACGAGGAGGCCTCCTT 335
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 GCCGGGCGGAGGCCAGAGGACCTGCAGGGCCAGGAGACGGGAAAACGCGGCCACGAGGAGGCCTCTT 287

Qy   336 CCAGGAGCGGACAGCACGCCCCAAAGAGGAGGAAAAGGAGAGATTCCGAGGAGGAGGAGAAGTC 395
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   288 CCAGGAGCGGACAGCACGCCCCAAAGAGGAGGAAAAGGAGAGATTCCGAGGAGGAGGAGAAGTC 347

Qy   396 GAAGCGGCAGAAGAAACCCAGGTCATCCTCCTGCCTCTGTGGGGAGTC 455
         |||||||||||||||||||||||||||||||||||||||||||
Db   348 GAAGCGGCAGAAGAAACCAGGTCATCCTCCTGCCTCTGTGGGGAGTC 407

Qy   456 CCTGTCCGAGGAGGAACTGCCCCAGATCCTTGGACCCAGGTGGAGAGAAAAAAGAAGCTCAT 515
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   408 CCTGTCCGAGGAGGAACTGCCCCAGATCCTTGGACCCAGGTGGAGAGAAAAAAGAAGCTCAT 467

Qy   516 TGCCACCATCCGGAGCAAGCCCTCGCCCATGGCCGAAGAAGCTGACGAGCTCAGGGAGGC 575
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   468 TGCCACCATCCGGAGCAAGCCCTGGCCCATGGCGAAGAAGCTGACAGAGCTCAGGGAGGC 527

Qy   576 CCAGGAATTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAGGGGGAAAGGGAGCAACTATA 635
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   528 CCAGGAATTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAGGGGAAAGGCAAGCAACTATA 587

Qy   636 TGCCTACAAGATCGTGATGGCCCAAGAAATGGGTCAAAATTTAAGAGAGACTTTGATAATT 695
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   588 TGCCTACAAGATCGTGATGGCCCAAGAAATGGGTCAAAATTTAAGAGAGACTTTGATAATT 647

Qy   696 CAAGACTCAAATGTATCCCCTGGGAAATGAAGATCAAGGAGCATTGAAAGTCACTTTGGTTC 755
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648 CAAGACTCAAATGTATCCCCTGGGAAATGAAGATCAAGGAGCATTGAAAGTCACTTTGGTTC 707

Qy   756 TTCAGTGGCATCGTATTTCATTCTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTT 815
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   708 TTCAGTGGCATCGTATTTCATTCTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTT 767

Qy   816 TGGCTTAAATATTTGGTCTAGTCATAATCCCAGAGGTACTGATGGGCATGCCCTATGGGAG 875
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   768 TGGCTTAAATATTTGGTCTAGTCATAATCCCAGAGGTACTGATGGGCATGCCCTATGGGAG 827

Qy   876 TATTCCCAGAAAGACAGTGCCTCGGCCTGAGGAAGAAAAAGGCCATGATTTTTCTGTCCT 935
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828 TATTCCCAGAAAGACAGTGCCTCGGGCTGAGGAAGAAAAAGGCCATGATTTTTCTGTCCT 887

Qy   936 TTGGGATTTTGAGGGCTACTATATCAAGTACTCTCGACTCTTCTATGGGCTACTACAAACAA 995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   888 TTGGGATTTTGAGGGCTACTATATCAAGTACTCTCGACTCTTCTATGGGCTACTACAAACCA 947

Qy   996 GAGGACCATCGGGTGGCTGGCTGAGGTACCGGGCTGCCTATGGGTCTTACTTTATGGTGG 1055
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   948 GAGGACCATCGGGTGGCTGGCTGAGGTACCGGGCTGCCTATGGGTCTTACTTTATGGGTCAG 1007

Qy  1056 CTACCTGATCGGGGAATTCAGAGACAGCTGATAACAAATATCCATCACCACCAGCTT 1115
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1008 CGTGTTCGGCTCACAGCCTGATTATTGTCATTGGATGGGCCAGCAAATACCCAAGGAAG 1067

Qy  1116 CACAGGCGGAAGGGAGGGAGAGGTGACAACTTCACATTCACATTCAAGCATTCAAAGGT 1175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1068 CACAGGCGGAAGGGAGGGAGAGGTGACAACTTCACATTCACATTCAAGGATGTTCACCAGCTGGGA 1127

Qy  1176 CTACCTGATCGGGGAATTCAGAGACAGCTGATAACAAATATCCATCACCACCAGCTT 1235
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1128 CTACCTGATCGGGGAATTCAGAGACAGCTGATAACAAATATCCATCACCACCAGCTT 1187

Qy  1236 CAAGGAATCAAATAGTGGATGAACAAGAGTAACAAAGAGAAGAAAATATCCATCTGACAAG 1295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1188 CAAGGAATCAAATAGTGGATGAACAAGAGTAACAAAGAGAAGAAAATATCCATCTGACAAG 1247

Qy  1296 ATTTCTTCGTGTCCTGGGCCAACTTTCTCATCACATCTGCTGTTGTGTGGGAAGTGGGTACTT 1355
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1248 ATTTCTTCGTGTCCTGGGCCAACTTTCTCATCACATCTGCTGTTGTGTGGGAAGTGGGTACCT 1307

Qy  1356 CATTTACTTTGTGGTTAACGGATCTCAGCAATTCTCCAAAAATGCAGAATCTCAGCTGGTA 1415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1308 CATTTACTTTGTGGTTAACGGATCTCAGCAATTCTCCAAAAATGCAGAATCTCAGCTGGTA 1367

Qy  1416 TGAAAGGAAATGAGGTAGAGATCGTGATGTCCCGTGCTTGGAAATGTTTTGTCCCCTCTGTT 1475
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1368 TGAAAGGAAATGAGGTAGAGATCGTGATGTCCCGTGCTTGGAAATGTTTTGTCCCCTCTGTT 1427

Qy  1476 TGAAACCATCGGCTGCCCTGGAGAATTACCACCCCACCACCACTGGACTGAAGTGGCAGCTGGG 1535
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1428 TGAAACCATCGGCTGCCCTGGAGAATTACCACCCCACCACCACTGGACTGAAGTGGCAGCTGGG 1487

Qy  1536 ACGGATCTTGCACTCTTCCTGGGGAACCTCTACACATTTCTCTTGGCCCTGATGGATGA 1595
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1488 ACGGATCTTGCACTCTTCCTGGGGAACCTCTACACATTTCTCTTGGCCCTGATGGATGA 1547

Qy  1596 CGTCCACCTCAAGCTTGCTAATGAACAATAAAGAACATCACTCACTGGACTCTGTT 1655
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1548 CGTCCACCTCAAGCTTGCTAATGAACAATAAAGAACATCACTCACTGGACTCTGTT 1607

Qy  1656 TAACTATTACAACTCTTCTGGTTGGAACGAGAGTGTCCCCGAGAGTGTCCCCGAGACCCTGC 1715
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1608 TAACTATTACAACTCTTCTGGTTGGAACGAGAGTGTCCCCGAGACCACCCCTGCACCCCTGC 1667

Qy  1716 AGATGTGCCCCGCGGGGTTCTTGCTGGGGACAGCTGTGGGGCCATTGAATTCATGAGGCTGAC 1775
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1668 AGATGTGCCCCGCGGGGTTCTTGCTGGGGACAGCTGTGGGGCCATTGAATTCATGAGGCTGAC 1727
```

Qy   1776 GGTGTCTGACATCTGGTAAGGTACAATCACCATCCTCGTCTGGGGGCTTG 1835
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1728 GGTGTCTGACATGCTGGTAAGGTACAATCACCATCCTCGTCTGGGGGCTTG 1787

Qy   1836 TTTTGTGCCGGTTCATGAACTACTGCTGGTTGGGACTTGGACGGCTGGATT 1895
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1788 TTTTGTGCCGGTTCATGAACTACTGCTGCTGGGACTTGGACGGCTTCCTTCATA 1847

Qy   1896 TGCCTGAGTTTGATTATTAGTTGGAAAATGTGCTGGTTTGATCTTCAACCAAGGAATGATCTG 1955
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1848 TGCCTGAGTTTGATTATTAGTTGGAAAATGTGCTGGTTTGATCTTCAACCAAGGAATGATCTG 1907

Qy   1956 GATGGGCTCCTTCTACGTCCAGGCCTGGTGGGCATTAATGTCGCGGCCTGCCTC 2015
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1908 GATGGGCTCCTTCTATGCTTCACAAGCCTGGTGGGCATTAATGTCGCGGCCTGCTGACCTC 1967

Qy   2016 CATGTACTTCCAGTGCTGCTGGGGGTGATGAGACAGACGGTACCCGCGTGTTCAA 2075
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1968 CATGTACTTCCAGTGCTGGGGGTGATGAGACAGCAGACGGTACCCGCGTGTTCAA 2027

Qy   2076 AGCCTCCCGATCCAACAACTTCTACATGGGGACCTCCTGCTGCTGCTCTTCCTCAGCCT 2135
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2028 AGCCTCCCGATCCAACAACTTCTACATGGGGACCTCTGCTGCTGGTGCTTCTTCCTCAGCCT 2087

Qy   2136 CCTGCGCGGTGGCCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGGGGCCGTTCAG 2195
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2088 CCTGCGCGGTGGCCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGGGGCCGTTCAG 2147

Qy   2196 TGGGAAAAACAGAATGTACGGATGTCTCCTCCAAAGAGACCATTGAAAAGCATTCCCAACTT 2255
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2148 TGGGAAAAACAGAATGTACGGATGTCTCCTCCAAAGAGACCATTGAAAAGCATTCCCAACTT 2207

Qy   2256 CCTGGGCAAGATCTTTGCTTTCCTCCCAATCCAGCCCTGATCATCCCAGCCATCCTGCT 2315
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2208 CCTGGGCAAGATCTTTGCTTTCCTCCCAATCCAGCCCTGATCATCCCAGCCATCCTGCT 2267

Qy   2316 GATGTTCTTGGCCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGACTAATGC 2375
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2268 GATGTTCTTGGCCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGACTAATGC 2327

Qy   2376 AGGCAAAGCCACACAGCAGAGATTCAGAGACACACTTAAAGCAGCTCAAAAATGCCAC 2435
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2328 CCAGCTGAGGAAGAAAATCCAAGTGCTCCGTGAAGTTGAGAGAGTCACAAATCTGTAAA 2387

Qy   2436 AGGCAAAGCCACACAGCAGAGATTCAGAGACACACTTAAAGCAGCTCAAAAATGCCAC 2495
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2388 AGGCAAAGCCACACAGCAGAGATTCAGAGACACACTTAAAGCAGCTCAAAAATGCCAC 2447

Qy   2496 CCAGCTGCCAACTCACCAAGGAAGAGAGACCACTCCTCCTCCTCCGCCAGCCAAAGCCAGGCCAT 2555
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2448 CCAGCTCCAACTCACCAAGGAAGAGAGACCACTCCTCCTCCGCCAGCCAAAGCCAGGCCAT 2507

Qy   2556 GGACAAGAGAGGGCAGGGGCCCCTGGGAACTTCCAAATTCTGCCACGAGGACCACACTGCCTGC 2615
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2508 GGACAAGAGAGGGCAGGGGCCCTGGGAACTTCCAAATTCTGCCACGAGGACCACACTGCCTGC 2567

Qy   2616 CTCTGGACAACCTTCTCTATATCTCGGCCCCCCTGGAATCGGACCAGATTCTGGCACGCGCCCC 2675
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2616 CTCTGGACAACCTTCTCTATATCTCGGCCCCCCTGGAATCGGACCAGATTCTGGCACGCGCCCC 2675

Db   2568 CTCTGGACACCTTCCTATATCTCGGCCCCCCTGGAATCGGACCAGATTCTGGCACGCGCCCCCACTG 2627

Qy   2676 ATCTCAGACTCATCCGTGGAGGTCAGCCTCTGGAAAGAGACTTCCCACTG 2735
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2628 ATCTCAGACTCATCCCTGGAGGTCAGCCTCTGGAAAGAGACTTCCCACTG 2687

Qy   2736 ACGGCTAGGACTCAGGGAGGCCTGGACCCTAGGGCCTGATCCTCAAAGTACCCAGTTCAC 2795
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2688 ACGGCTAGGACTCAGGGAGGCCTGGACCCTAGGGCCTGATCCTCAAAGTACCCAGTTCAC 2747

Qy   2796 ACATACCAAAACCAAGGTTCTCTCCCCTCTTCCTCTCACATACATGCTCTGTCTCTCTC 2855
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2748 ACATACCAAAACCAAGGTTCTCTCCCCTCTTCCTCTCACATACATGCTCTGTCTCTCTC 2807

Qy   2856 TTGGAATGCATGAACTTTGATTCCTTCAGGGCCCTTGTCGACGTACCGAAGGAGAAGAGACAG 2915
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2808 TTGGAATGCATGAACTTTGATTCCTTCAGGGCCCTTGTCAGCTAACGGAAGGAGAAGAGACAG 2867

Qy   2916 TGGCTTCACCTGTCCTCTTTAGGGAAGAGCTGGAGCCCATCATCTGCACTAACTGCCTCCCAAAT 2975
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2868 TGGCTTCACCTGTCCTTTAGGGAAGGCTGGAGCCCATCCTGCACTAACTGCCTCCCAAAT 2927

Qy   2976 ATCTTGGTTCAGACAGCTCTGAACCCCAGCGCTCACAGTGGGTCGACCTTGCCTCCCGATTT 3035
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2928 ATCTTGGTTCAGACAGCTCTGAACCCCAGCGCTCACAGTGGGTCGACCTTGCCTCCCGATTT 2987

Qy   3036 TCCGGAGTTGGGGAGAGGGCCATGACCACCCCTCCTAGACATTTTTCCATGGGATACAGTTAG 3095
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2988 TCCGGAGTTGGGGAGAGGGCCATGACCACCCCTCCTAGACTTTTCCATGGGATACAGTTAG 3047

Qy   3096 GACACGGGGTTCTGCCACGCTTCCCTAACGAGGAGGGGGGATGGAGAAGGGGCCTACATTTCT 3155
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3048 GACACGGGGTTTCTGCCACGCTTCCCTAACGAGGAGGGGGGATGGAGAAGGGGCCTACATTTCT 3107

Qy   3156 CAATCCAGAGGAAG 3169
           ||||||||||||||
Db   3108 CAATCCAGAGGAAG 3121

RESULT 2
AAS92296
ID   AAS92296 standard; cDNA; 5027 BP.
XX
AC   AAS92296;
XX
DT   13-FEB-2002 (first entry)
XX
DE   DNA encoding novel human diagnostic protein #28100.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX

PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; AB028109.
XX
PS   Claim 1; SEQ ID NO 28100; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (III). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (II) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (III) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (III). (I) and (III) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AA564197-AA594564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5027 BP; 1316 A; 1289 C; 1339 G; 1083 T; 0 U; 0 Other;

Query Match   72.4%; Score 2294.6; DB 5; Length 5027;
Best Local Similarity   90.9%; Pred. No. 0;
Matches 2545; Conservative   0; Mismatches   59; Indels 195; Gaps   2;

Qy   93 CACAGGTGACAGGGAGGAAGGAGATCCTCAAGCAGCAGCGAGGGGAC 152
           | ||||||||||||||||||||||||||||||||||||||||||||||||
Db   45 CTCAGGTGACAGGCTGGGAAGAGAGATCCTCAAGCAGCAGCGAGGGGAC 104

Qy   153 CCCAGGCAGGCCGCGGAGCTCAGCGAAGCCAGGAAGCGCGCCGCGGGGGCCAGCCCAAGCCC 212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   105 CCCAGGCAGGCCGCGGAGCTCACGGAAGCCAGGAAGCGCGCCGCGGGGGCCAGCCCAAGCCC 164

Qy   213 GGGGTCTCCCCGCGGAAGCAAAACAGGGCGGCCAGGAGACAGCAGGAGACTGGGGGAGCA 272
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   165 GGGGTCTCCCCGCGGAAGCAAAACAGGGCGGCCAGGAGACAGCAGGAGACTGGGGGAGCA 224

Qy   273 GGAGCGGGGGGCCAGGCGAGGAGGAGGAGGAGGAGGAGAAAACAGGCGCAGGAGGAGGAGGAGGAGGAGCTC 332
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   225 GGAGCGGGGGGCGAGGCGAGGAGGAGGAGGAGGACCTGGGGGAGCTC 284

Qy   333 CTTCCAGGAGGCGACGCAGCCCCAAAGAGGGGAAAGAGGATTCCGGAGGAGGAGGAGGAA 392
           |||||||||||||| ||||||||||||||||||||||| ||||||||
Db   285 CTTCCAGGAGCGGGACGCAGCCCAAAGAGGGAAAGAGGATTCCGGAGGAGGAGGAGGAA 344

Qy   393 GTCGAAGCGGGCAGGAAGAAAACCCAGTGCATCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGA 452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   345 GTCGGAAGCGGGCAGAGAGAAAACCCAGTGCATCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGA 404

Qy   453 GTCCCTGTCCCAGGAGGAACTGGCCCCACAATCCTTGGAGCAGGTTGGAGAAAAAAGAAGCT 512
           ||||||| |||||||||||||||||||||||||||||||||||||||||| |||||||
Db   405 GTCCCTGTCCGAGGAGGAACTGGCCCGGAGGTTGGAGAAAAAAGAAGCT 464

Qy   513 CATTGCCACCATGCGGAGCAGCCCCTGGCCATGGCGGAAGAAGCTGACAGAGCTCAGGGA 572
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465 CATTGCCACCATGCGGAGCAGCCCCTGGCCATGGCGGAAGAAGCTGACAGAGCTCAGGGA 524

Qy   573 GGCCCAGGGAATTGTGGGAGAAGTATGAAGGTGCCCTTGGGAAAGGGGAGAAAAGGCAAGCAACT 632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525 GGCCCAGGAAATTGTGGGAGAAGTATGAAGGGCCCTTGGGAAAGGGGAGAAAAGGCAAGCAACT 584

Qy   633 ATATGCCTACAAGATGCTGATGGGCCAAGAAAATGGGTCAAAATTAAGAGAGACTTTGATAA 692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585 ATATGCCTACAAGATGCTGATGGCCAAGAAAATGGGTCAAATTTAAGAGAGACTTTGATAA 644

Qy   693 TTTCAAGACTCAATGTATCCCCTGGGGAAATGAAGATCAAGGACATTGAAAGTCACTTTGG 752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   645 TTTCAAGACTCAATGTATCCCCTGGGGAAATGAAGATCAAGGACACATTGAAAGTCACTTTGG 704

Qy   753 TTCTTCAGTGGCATCGTATTTCATCTTTCTCCGATGTATGGAGTTAACCTTGTCCT 812
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   705 TTCTTCAGTGGCATCGTATTTCATCTTTCTCCGATGAATGTATGGAGTTAACCTTGTCCT 764

Qy   813 TTTTGGCTTAATATTTGGTTCTAGTCATAAATCCCAGAGGTACT---------------- 854
           |||||||||||||||||||||||||||||||||||| -
Db   765 TTTTGGCTTAATATTTGGTTCTAGTCATAAATCCCAGAGAGTGTCTACGGTGATCCCTGAGGA 824

Qy   855 ----------------GATGGGCATGCCCTATGGGAGTATTCCCAGAAAGA 889
                           | ||||| | ||| || ||
Db   825 ACCTTCAGTTATGCTGCAGAGCTGGCTGGCAAGGCCCCACTGGATGACAGCAGTTTATGTA 884

Qy   890 CAGTGCCTCGGGCCTGAGGAAGAAAGGCCATGGATTTTTTCT------------------- 930
             | | ||| ||||||| || |||||||||||||||||| -
Db   885 CTTCTTCTTCCAACACTGGATCCTACGGTCTAGGTTTTGACCAAGGCTACAATTATCTTGA 944

Qy   931 -- 930
           -
Db   945 GGCTGAACTGAAGAAGATCCGCTTCCAAGCTCACTCACATGGCTACTGGCCAGATCTCAGA 1004

Qy   931 -- 930
           -
Db   1005 CCCAGGCAGGCCGCGGAGCTCACGGAAGCCAGGAAGCGCGCCGCGGGGGCCAGCCCAAGCCC 1064

```
Db  1005  AGATACAATTTCAAGCTTACTCACGTTGGCTTCTTGGGCAGCCCTCAGAAAATCTGCTTCCAA  1064

Qy   931  ------------GTCCTTTGGGATTTTGAGGGCTATATCAAGTACTCTGCACTCTTCTA        977
              |  |       |||||
Db  1065  CCTTACTTATGTGGCTGTTCCCAAGGTTCAGGGGCTATATCAAGTACTCTGCACTCTTCTA   1124

Qy   978  TGGCTACTACAACACCAGAGGACCATCGGGTGGGTGGGTACCGGCTACTATGGCTTA        1037
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  1125  TGGCTACTACAACACCAGAGGACCATCGGGTGGGTGAGGGTACCGGCTACTATGGCTTA     1184

Qy  1038  CTTTATGGTTGGTGGGGGGTCAGGGTCAGGGCTGTTCGGGCTACAGCCTGATTATTGTCATTCGATCGATGGC  1097
          ||||||||||||  ||||||||| |||||||||||||||||||||||||||||||||||||||
Db  1185  CTTTATGGTTGGGGGGTCAGGGCTGTTCGGGCTACAGCCTGATTATTGTCATTCGATCGATGGC   1244

Qy  1098  CAGCAATACCCAAGGAAGGACAGGGGGAGGGAGAGTGCAACTTCACATTCAGCTTCAA       1157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245  CAGCAATACCCAAGGAAGGACAGGGGGAGGGAGAGTGCAACTTCACATTCAGCTTCAA       1304

Qy  1158  GATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACACAGCTGATAAACAAATATGC  1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1305  GATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACACAGCTGATAAACAAATATGC  1364

Qy  1218  ATCCATCACCACCACCAGCTTCAAAGGAATCAAATAGTAGTAGCAAGAAGAAGTAACAAGAAGA  1277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1365  ATCCATCACCACCACCAGCTTCAAAGGAATCAAATAGTAGTAGCAAGAAGAAGTAACAAGAAGA  1424

Qy  1278  AAATATCCATCTGACAAGATTTCTTCGTCGTGTCCTGGGCCACACTTTCTCATCATCTGCTGTTT  1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425  AAATATCCATCTGACAAGATTTCTTCGTCGTGTCCTGGGCCACACTTTCTCATCATCTGCTGTTT  1484

Qy  1338  GTGTGGAAGTGGGGTACCTCATTTACTTTGTGGTTAAGCGAATCTCAGCAATTCTCCAAAAT   1397
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Db  1485  GTGTGGAAGTGGGGTACCTCATTTACTTTGTGGTTAAGCGAATCTCAGCAATTCTCCAAAAT   1544

Qy  1398  GCAGAATGTCACCTGGTATGAAAGGAATGAGTGTAGTAGTCGTGATGTCCCTGCTTGGAAT    1457
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Db  1545  GCAGAATGTCACCTGGTATGAAAGGAATGAGTGTAGTAGTCGTGATGTCCCTGCTTGGAAT    1604

Qy  1458  GTTTTGTCCCCCTCTGTTTGAAAACCATCGCTGCCCTGGGAGAATTACCACCCACGCACTGG  1517
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Db  1605  GTTTTGTCCCCCTCTGTTTGAAAACCATCGCTGCCCTGGGAGAATTACCACCCACGCACTGG  1664

Qy  1518  ACTGAAGTGGGCAGCTGGGACGGGCATCTTTGCACTCTTCCTGGGGAACCTCTACACCATTTCT  1577
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Db  1665  ACTGAAGTGGGCAGCTGGGACGGGCGATCTTTGCACTCTTCCTGGGGAACCTCTACACCATTTCT  1724

Qy  1578  CTTGCCCTGATGGATGAGGTCCACCTCAAGGTTGCTGCTAATGAAGAAGCAATAAAGAACAT   1637
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Db  1725  CTTGGCCCTGATGGATGAGGTCCACCTCAAGGTTGTGCTAATGAAGAAGCAATAAAGAACAT   1784

Qy  1698  ACCACCCCTGCACCCTGCAGAGTGCCCCGGGGTTCTTGCCTGGGAGACAGCTGTGGGCAT    1757
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Db  1785  CACTCACTGGACTCTGTTTAACTATTACAACTCTTCTGGTTGAAACGAGAGTGTCCCCCG      1844


Db  1845  ACCACCCCTGCACCCTGCAGAGTGCCCCGGGGTTCTTGGGGAGACAGCAGCTGTGGGCAT     1904

Qy  1758  TGAATTCATGAGGGCTGACGGGTGTCTTGACATGCTGGTGGTAACGGTACATCACCATCCTGCTGCTGGG  1817
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Db  1905  TGAATTCATGAGGGCTGACGGGTGTCTTGACATGCTGGTGGTAACGGTACATCACCATCCTGCTGGGG  1964

Qy  1818  GGACTTCCTACGGGCTTGTTTTTGTCGCGGTTCATGAACTACTGCTGGTGCTGGGACTTGGA   1877
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Db  1965  GGACTTCCTACGGGCTTGTTTTTGTCGCGGTTCATGAACTACTGCTGGTGCTGGGACTTGGA   2024

Qy  1878  GGCTGGGATTTCCTTCATATGTGCTGAGTTTGATATTAGTGGAAAATGTGCTGGGTTTGATCTT  1937
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Db  2025  GGCTGGGATTTCCTTCATATGTGCTGAGTTTGATATTAGTGGAAAATGTGCTGGGTTTGATCTT  2084

Qy  1938  CAACCAAGGAATGAATCTGGATGGGCTCCTTCTTCATCCTCCAGGCCTGGGTGGGGCCATTAAATGT  1997
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Db  2085  CAACCAAGGAATGAATCTGGATGGGCTCCTTCTTCATCCTCCAGGCCTGGGTGGGGCCATTAAATGT  2144

Qy  1998  GCTGCCCCTGCTGACCTCCATGTCACTTCCTTACTTCCCAGTGCTGGGGGGTGATGAGCGAGAACGTACC  2057
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Qy  2058  CCATGAACGGGTGTTCAAAAGCCTCCCGATCCCAACAACTTCTACAGTGGGCCTCCTGCTGCT  2117
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Db  2205  CCATGAACGGGTGTTCAAAAGCCTCCCGATCCCAACAACTTCTACAGTGGGCCTCCTGCTGCT  2264

Qy  2118  GGTGCTCTTCCTCAGCCTCTCCGGGTGGGCTACCATCCACCACCATGTCCCTCCCACCCTCCTT  2177
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Db  2265  GGTGCTCTTCCTCAGCCTCTCCGGGTGGGCTACCATCCACCACCATGTCCCTCCCACCCTCCTT  2324

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Db  2385  AAACGATTTCCCAACCTTCCTGCTGCTTCCTTGGGGCATTTTACTACCTGAACTCAGGGCCTGAT  2444

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Db  2445  CATCCCAGCCATCCTGCTGATGTTCTTTGGGCCATTTACTACGTACCTCAGTTTCCAAAAG    2504

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Db  2505  CCTTTCCCGAGCTAATGCCCAGCTGAGGAAGAGAAAATCCAAGTGCTTCGCGTGAAGTTGAGA   2564

Qy  2418  GAGTCACAAATCTGTAAAAGGCAAAAGCCACACAGCCAGATTCAGAGGACGACACAGCCTAAAAG  2477
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Db  2565  GAGTCACAAATCTGTAAAAGGCAAAGCCACAGCCAGATTCAGAGGACAATAAAAG          2624

Qy  2478  CAGCTCCAAAAATGCCACCCAGCTCCAACTCACCAAGCCAGACAGCTCCTCCTGC          2537
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Db  2625  CAGCTCCAAAAATGCCACCCAGCTCCAACTCACCAAGCCAGACAGCTCCTCCTGC          2684

Qy  2538  CAGCCAAAGCCAGCCATGGACAAGAAGCGAGGGGCCCCTGGGACCTCCCAATTCTGCCAG       2597
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Db  2685  CAGCCAAAGCCAGCCATGGACAAGAAGCGAGGGGCCCCTGGGACCTCCCAATTCTGCCAG       2744
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Qy   2598 CAGGACCACACTGCCTTGCCTTCTGGACACTTTCCTATATATCTCGGCCCCCTGGAATCGGACC 2657
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Db   2745 CAGGACCACACTGCCTTGCCTTCTGGACACTTTCCTATATATCTCGGCCCCCTGGAATCGGACC 2804

Qy   2658 AGATTCTGGCCACGCCCCATCTCAGACTCATCCGTGGAG 2696
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Db   2805 AGATTCTGGCCACGCCCCATCTCAGACTCATCCGTGGAG 2843

Search completed: November 30, 2005, 05:16:58
Job time : 1716 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 05:17:05 ; Search time 569 Seconds
                                                (without alignments)
                                                9899.988 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgaccatgag.........atttctcaatccagaggaag 3169

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   Issued_Patents_NA:*
           1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
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           5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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           9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | Score | Query Match | Length | DB | ID | Description |
No.		Score						
c	1		96	3.0	7218	2	US-08-232-463-14	Sequence 14, Appl
c	2		76.4	2.4	2001	3	US-09-799-451-695	Sequence 695, App
c	3		51.6	1.6	7218	3	US-08-232-463-14	Sequence 14, Appl
c	4		50	1.6	1926	3	US-09-249-585A-2	Sequence 2, Appli
c	5		50	1.6	1926	3	US-09-410-399-3	Sequence 3, Appli
c	6		50	1.6	2580	3	US-09-050-863-2	Sequence 2, Appli
c	7		50	1.6	2580	3	US-09-359-081-2	Sequence 2, Appli
c	8		50	1.6	5452	2	US-09-130-114-1	Sequence 1, Appli
c	9		50	1.6	8705	3	US-09-647-344A-14	Sequence 14, Appl

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 06:00:20 ; Search time 2220 Seconds
                (without alignments)
                11804.351 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgctgaccactgag..........atttctcaatccagaggaag 3169

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_NA_Main:*
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            4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
            5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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            7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
            8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3169	100.0	3169	9	US-10-792-307-3	Sequence 3, Appli
2	3074	97.0	3121	8	US-10-487-887-3	Sequence 3, Appli
3	2294.6	72.4	5027	9	US-10-450-763-28100	Sequence 28100, A
4	2293	72.4	4895	6	US-10-115-831-134	Sequence 134, App
5	1957.6	61.8	3216	9	US-10-487-887-7	Sequence 7, Appli
6	1957.6	61.8	3216	9	US-10-792-307-7	Sequence 7, Appli
7	816.8	25.8	2895	8	US-10-487-887-5	Sequence 5, Appli
8	816.8	25.8	2895	9	US-10-792-307-5	Sequence 5, Appli
10	50	1.6	9600	3	US-08-910-647-1	Sequence 1, Appli
11	50	1.6	9600	2	US-09-620-925-1	Sequence 1, Appli
12	50	1.6	10596	2	US-07-884-811-15	Sequence 15, Appl
13	50	1.6	10596	2	US-07-885-971-15	Sequence 15, Appl
14	50	1.6	10596	2	US-08-087-783A-15	Sequence 15, Appl
15	50	1.6	10596	2	US-08-194-087-15	Sequence 15, Appl
16	50	1.6	10596	2	US-08-194-088B-15	Sequence 15, Appl
17	50	1.6	10596	6	PCT-US93-04648-15	Sequence 15, Appl
18	50	1.6	16080	3	US-09-724-566A-48	Sequence 48, Appl
19	50	1.6	16080	3	US-09-471-669A-48	Sequence 48, Appl
20	48	1.6	16442	3	US-09-781-891-208	Sequence 208, App
21	48	1.6	16442	3	US-09-618-166-208	Sequence 208, App
22	48	1.5	53526	3	US-08-658-136-2	Sequence 2, Appli
23	48	1.5	53577	3	US-08-658-136-1	Sequence 1, Appli
24	48	1.5	53577	3	US-08-460-215A-1	Sequence 1, Appli
25	47.8	1.5	507	3	US-09-489-039A-1200	Sequence 1200, Ap
26	47.8	1.5	516	3	US-09-489-039A-1064	Sequence 1064, Ap
27	47.8	1.5	537	3	US-09-489-039A-1065	Sequence 1065, Ap
28	47.8	1.5	549	3	US-09-489-039A-1130	Sequence 1130, Ap
29	47.8	1.5	558	3	US-09-489-039A-1011	Sequence 1011, Ap
30	47.8	1.5	609	3	US-09-489-039A-1177	Sequence 1177, Ap
31	46.8	1.5	1926	3	US-09-249-585A-4	Sequence 4, Appli
32	46.8	1.5	1931	2	US-09-130-114-2	Sequence 2, Appli
33	46.6	1.5	6644	3	US-08-875-435B-5	Sequence 5, Appli
34	46.2	1.5	39489	3	US-09-949-016-13886	Sequence 13886, A
35	45.8	1.5	2093	3	US-10-104-047-1666	Sequence 1666, Ap
36	44.8	1.4	3489	3	US-09-298-568-1	Sequence 1, Appli
37	44.8	1.4	3489	3	US-08-728-323A-1	Sequence 1, Appli
38	44.8	1.4	3489	3	US-09-410-399-1	Sequence 1, Appli
39	44.8	1.4	3489	3	US-09-894-273-1	Sequence 1, Appli
40	44.8	1.4	32207	2	US-08-770-379-20	Sequence 20, Appl
41	44.8	1.4	32207	3	US-08-757-669A-20	Sequence 20, Appl
42	44.8	1.4	32207	3	US-09-230-371A-20	Sequence 20, Appl
43	44	1.4	1408	2	US-08-222-124-10	Sequence 10, Appl
44	44	1.4	1408	2	US-08-842-657A-10	Sequence 10, Appl
45	44	1.4	1414	2	US-08-222-124-9	Sequence 9, Appli

Search completed: November 30, 2005, 12:49:43
Job time : 572 secs

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 11   591.8   18.7   2560   6   US-10-108-260A-342      Sequence 342, App
 12   193     6.1    5929  10   US-11-097-143-6038      Sequence 6038, Ap
 13   154.4   4.9    1060   6   US-10-027-632-122322    Sequence 122322,
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 15   104.6   3.3    1177   6   US-10-006-867-129       Sequence 129, App
 16   104.6   3.3    1177   5   US-10-052-586-381       Sequence 381, App
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 18   104.6   3.3    1177   5   US-10-063-551-129       Sequence 129, App
 19   104.6   3.3    1177   5   US-10-174-590-381       Sequence 381, App
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 36   104.6   3.3    1177   5   US-10-176-757-381       Sequence 381, App
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 41   104.6   3.3    1177   5   US-10-173-700-381       Sequence 381, App
 42   104.6   3.3    1177   5   US-10-174-572-381       Sequence 381, App
 43   104.6   3.3    1177   5   US-10-174-579-381       Sequence 381, App
 44   104.6   3.3    1177   5   US-10-174-582-381       Sequence 381, App
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ALIGNMENTS

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Best Local Similarity   100.0%;  Pred. No. 0;
Matches  3169;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 GCAGTGCTGCTGACCATGAGCCACCAGGTAAAGGAAGGCACGAGGCGGA 60
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Qy    61 GTGAAAGGCGGGGGGTGAAGAGGCGCTCTTCCACACACAGGTGACAGAGATCC 120
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Qy   121 TCAAGCAAGCGGGCGCTCAAAGCCGAGGGGGGGACCCCAAGCGGGGAGC 180
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Qy   181 CAGAAGGACGCGCGGCCGGCAGCCCAAGCCGCGGGGGGTCTCCCGGGGAGGGAACAGGG 240
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Qy   241 CCGAGGAGACACAGAGAGCTGGGGGAGCAGGAGGCCAGAGAGGACTGC 300
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Qy   301 GAGGGCCAGGAGAAAGCGGACGAGAGGGCCTCCTTCCAGGAGGGGGACCCCAAAG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   361 AGGGAAAAGGAGATTCCGAGGAGGAGGAGGAAGTCGAAGCGGCAGAACCCAGGTCA 420
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Qy   421 TCCTCCTTGGCCTCCAGTGCCTCGTGTGGGGAGTCCCTGTCCGAGGAGGAAACTGGCCCAG 480
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Qy   481 ATCCTGGACGCAGGTGGAGAAAAAGAAGCTCATTGCCACCATGCGGAGCAAGCCCTG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   541 CCCATGGCCGGAGAAGCTGACGAGCTCAGGGAGGCCCAGGGAATTTGTTGGAGAGTATGAA 600
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Db   541 CCCATGGCCGGAGAAGCTGACGAGCTCAGGGAGGCCCAGGGAATTTGTTGGAGAGTATGAA 600

Qy   601 GGTGCCTTGGGAAAGGGGAAAGGCAAGCAACTATATGCCTACAAAGATGCTGCCCAG 660
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Db   601 GGTGCCTTGGGAAAGGGGAAAGGCAAGCAACTATATGCCTACAAAGATGCTGCCCAG 660

Qy   661 AAATGGGTCAAATTTAAGAGAGACTTTGATAATTTCAAGAACTCAATGTATCCCTGGGAA 720
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Db    661 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    721 ATGAAGATCAAGGACATTGAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATCTTT  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATGAAGATCAAGGACATTGAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATCTTT  780

Qy    781 CTCCGATGGATGATGATGGAGTTAACCTTGTCCTTTTTGGGCTTAATATTGGTTCTTAGTGTATCATA  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTCCGATGGATGATGATGGAGTTAACCTTGTCCTTTTTGGGCTTAATATTGGTTCTTAGTGTATCATA  840

Qy    841 ATCCCAAGAGGTACTGATGGGCATGGGCCCTATGGGGAGTATTCCCAGAAAAGACAGTTGCCTCGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    901 GCTGAGGGAAGAAAAGGCCATGGATTTTTCTGTCCCTTTGGGGCTATTTGAGGGCTATATCAAG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCTGAGGAAGAAAAGGCCATGGATTTTTCTGTCCCTTTGGGGGCTATTTGAGGGCTATATCAAG  960

Qy    961 TACTCTGCACTCTTCTATGGCTACTACAGCAGCACCAGAGGACCATCGGGGTGGCTGAGGTAC  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TACTCTGCACTCTTCTATGGCTACTACAACCAGAGGACCATCGGGGTGGCTGAGGTAC  1020

Qy   1021 CGGCTGCCTATGGCTTACTTTATGGGTGGGGGTCAGCCGTGTTCGGGCTACAGCCCTGATTATT  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CGGCTGCCTATGGCTTACTTTATGGGTGGGGGTCAGCCGTGTTCGGGCTACAGCCCTGATTATT  1080

Qy   1081 GCTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGCGGGGAGAGAGTGACAAC  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GCTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGCGGGGAGAGAGTGACAAC  1140

Qy   1141 TTCACATTCAGCTTCAAGATGTTCACGCAGGCACTCACCTGATCGGGAATTCAGAGACA  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTCACATTCAGCTTCAAGATGTTCCACGCAGGCACTCACCTGATCGGGAATTCAGAGACA  1200

Qy   1201 GCTGATAAACAAATATGCATCCATCACCACCCAGCTTCAAGGAATCAATAGTGGATGAACAA  1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCTGATAAACAAATATGCATCCATCACCACCCAGCTTCAAGGAATCAATAGTGGATGAACAA  1260

Qy   1261 GAGAGTAACAAAGAGAGAAAATATCCATCTGACAAGAATTCTTCGTGTCCTGGCCCAACTTT  1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAGAGTAACAAAGAGAGAAAATATCCATCTGACAAGAATTCTTCGTGTCCTGGCCCAACTTT  1320

Qy   1321 CTCATCATCTGCTGTTTGTGTGGAAGTGGGGTACCTGCATTTACTTTGTGGTTAAGGCGATCT  1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTCATCATCTGCTGTTTGTGTGGAAGTGGGGTACCTGCATTTACTTTGTGGTTAAGGCGATCT  1380

Qy   1381 CAGCAATTCTCCAAAATGCAGAATGTCAGCTGTATAGAAAGGAATGAGGTAGAGATCGGTG  1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CAGCAATTCTCCAAAATGCAGAATGTCAGCTGTATAGAAAGGAATGAGGTAGAGATCGGTG  1440

Qy   1441 ATGTCCCTGCTTGGAAATGTTTTGTTGTCCCCTCTGTTTGAAAACCATCGCTCGCTGCCCTGGAGAAT  1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 ATGTCCCTGCTTGGAAATGTTTTGTTGTCCCCTCTGTTTGAAAACCATCGCTCGCTGCCCTGGAGAAT  1500
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Db   1501 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TACCACCCACGCACTGGACTGAAGTGGCAGCGTGGACCGGCATCTTTGCACTCTTCCTGGGG  1560

Qy   1561 AACCTTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTTCAAGCTTGCTTAATGAA  1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AACCTTCTACACATTTCTCTTGGCCCTGATGGATGACGTCCACCTTCAAGCTTGCTTAATGAA  1620

Qy   1621 GAGACAATAAAAGATCACTACTCACTGTCTGTTTACTATTACAAACTCTTCTGGTTGG  1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGACAATAAAAGAACATCACTCACTGGACTCTGTTTAACTATTACAAACTCTTCTGGTTGG  1680

Qy   1681 AACGAGAGTGTCCCCGGACCACCCCCTCGACCCCTCGCAGATGTGCCCCGGGGTTCTTGCTGG  1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 AACGAGAGTGTCCCCGGACCACCCCTCGACCCCTGCAACCCTGCAGATGTGCCCCGGGGTTCTTGCTGG  1740

Qy   1741 GAGACAGCAGCTGTGGGGCCATTGAATTCATGAGGGCTGACGGGTGTCTGACATGCTGGTAACGTAC  1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GAGACAGCAGCTGTGGGGCATTGAATTCATGAGGGCTGACGGGTGTCTGACATGCTGGTAACGTAC  1800

Qy   1801 ATCACCATCCTGCTGGGGACTTCCTACTGGGGGCTTGTTGTTTTGTCGGGTTCATGAACTACTGC  1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATCACCATCCTGCTGGGGACTTCCTACTGGGGGCTTGTTGTTTTGTCGGGTTCATGAACTACTGC  1860

Qy   1861 TGGTGCTGGGACTTGGGAGGGCTGGATTTCCTTCATATGCTGAGGTTGATATTAGTGGAAAT  1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGTGCCTGGGACTTGGAGCTGGGAGGGCTGGATTTCCTTCATATTGCTGAGGTTGATATTAGTGGAAAT  1920

Qy   1921 GTGGCTGGGGTTTGATCTTCAACCAAGGAATGATCGGAATGGGGCTCCTTCTATGCTCCAGGC  1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GTGCTGGGGTTTGATCTTCAACCAAGGAATGATCGGAATGGGGCTCCTTCTATGCTCCAGGC  1980

Qy   1981 CTGGTGGGGCATTAATGTGCTTGGGCCTGCTGACCTCCATGTACTTCCAGTGCTGGGCCGTG  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CTGGTGGGGCATTAATGTGCTTGGGCCTGCTGACCTCCATGTACTTCCAGTGCTGGGCCGTG  2040

Qy   2041 ATGGAGCAGCAACGTACCCCATGACCGTGTTGTTCAAAGCTCCCATCAAACAACTTCTAC  2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 ATGGACCAGCAACGTACCCCATGACCGTGTTGTTCAAAGCTCCCATCAAACAACTTCTAC  2100

Qy   2101 ATGGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCTCGCCGGGTGCCTACCACCATCATG  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCTCGCCGGGTGGCCTACACAGATCATG  2160

Qy   2161 TCCCTCCCACCCTCCTTTGACTGCGGCCGTTGCAGTGGGAGAAAAACAGAAGTACCGATGTC  2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TCCCTCCCACCCTCCTTTGACTGGGGGCCGTTCAGTGGGAAAAACAGAGAATGTACGATGTC  2220

Qy   2221 CTCCAAAGAGACCATTGAAAACGATTTCCCAACCTTCCTCGGCCAGAGATCTTTGCTTCCTC  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CTCCAAAGAGACCATTGAAAACGATTTCCCAACCTTCCTCGGCCAAGATCTTTGCTTCCTC  2280

Qy   2281 GCCAATCCAGGGCCTGATCATCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTTACCTG  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GCCAATCCAGGGCCTGATCATCCAGCCATCCTGCTGATGTTCTTGGGCCATTTACTTACCTG  2340

Qy   2341 AACTCAGTTCCAAAAGGCCTTCCCGGAGCTAATGCCCAGCTGAGGAAAAATCCAAGTG  2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AACTCAGTTCCAAAAGGCCTTCCCGGAGCTAATGCCCAGCTGAGGAAGAAAAATCCAAGTG  2400
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Query Match   97.0%; Score 3074; DB 8; Length 3121;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3074; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   96 AGGTGACAGGCGTGGGAAGGAGATCCTCAAGCAAGCGGGGCTCTCAAAGCCGAGGGGACCCC 155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   48 AGGTGACAGGCGTGGGAAGGAGATCCTCAAGCAAGCGGGGCTCTCAAAGCCGAGGGGACCCC 107

Qy   156 AGGCAGGCGCCGGAGCTCAGCGAAGCCAGAAGAGCGGCGCCCGGGGCGCCAAGCCCGGG 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   108 AGGCAGGCGCCGGAGCTCAGCGAAGCCAGAAGAGCGGCGCCCGGGGCGCCAAGCCCGGG 167

Qy   216 GTCTCCCCGGAGGAAGCAAAACAGGGCGCCAGGAGACACAGAGAAGAGACTGGGGGCCAGGA 275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   168 GTCTCCCCGGAGGAAGCAAAACAGGGCGCCAGGAGACACAGAGAAGAGACTGGGGGCCAGGA 227

Qy   276 GCGGGGGCCAGGCCAGCAGAGAGGCGCAGGGACGGAAAGACGCGCGACGAGAGGGCCTCCTT 335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   228 GCGGGGGCCAGGCCAGCAGAGAGGCGCAGGGACGGAAAGACGCGCGACGAGAGGGCCTCCTT 287

Qy   336 CCAGGAGCGGGACAGCGCCCAAAGAGGGAAAAAGAGAATTCCGAGGAAGGAGGAGAGTC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   288 CCAGGAGCGGGACAGCGCCCAAAGAGGGAAAAAGAGAATTCCGAGGAAGGAGGAGAGTC 347

Qy   396 GAAGCGGCAGAAGAAACCCAGGTCATCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGAGTC 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   348 GAAGCGGCAGAAGAAACCCAGGTCATCCTCCTTGGCCTCCAGTGCCTCTGGTGGGGAGTC 407

Qy   456 CCTGTCCGAGGAGGAACTGGCCCAGCAGGTGGAAGAAAAAAAAGAAAGCTCAT 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   408 CCTGTCCGAGGAGGAACTGGCCCAGCAGGTGGAAGAAAAAAAAGAAAGCTCAT 467

Qy   516 TGCCACCATGCCGACGAGGAACCCTGGCCCAGATCCTGAGCAGTGACGAGAGCTCAGGGAGGC 575

Qy 2401 CTCCGTGAAGTTGAGAAGAGACTCACAAATCTGTAAAAGGCAAACCACCAGCCAGAGATTCA 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2401 CTCCGTGAAGTTGAGAAGAGACTCACAAATCTGTAAAAGGCAAACCACCAGCCAGAGATTCA 2460

Qy 2461 GAGGACAACACCTAAAAGCAGCTCCAAAAATGCCACCCAGTCACCACCAAGGAAGAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461 GAGGACAACACCTAAAAGCAGCTCCAAAAATGCCACCCAGTCACCACCAAGGAAGAG 2520

Qy 2521 ACCACTCCTCCTTCCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGAAGGCGCCCTGGG 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2521 ACCACTCCTCCTTCCTGCCAGCCAAAGCCAGGCCATGGACAAGAAGAAGGCGCCCTGGG 2580

Qy 2581 ACCTCCAATTCTGCCAGCACAGGACCACACTGCCCTGCCTCTTGGACACCTTCTATATCTCGG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 ACCTCCAATTCTGCCAGCACAGGACCACACTGCCCTGCCTCTTGGACACCTTCTATATCTCGG 2640

Qy 2641 CCCCCTGGAATCGGACCAGATTCTGGCCAGGCCCCATCTCAGACTCATCCGTGGAGTCA 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641 CCCCCTGGAATCGGACCAGATTCTGGCCAGGCCCCATCTCAGACTCATCCGTGGAGTCA 2700

Qy 2701 GCCTCTGGAAAGAGTGCTCAGAGACACTCCCCACTGACGGGCTAGGACTCCAGGAGCCTCG 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2701 GCCTCTGGAAAGAGTGCTCAGAGACACTCCCCACTGACGGGCTAGGACTCCAGGAGCCTCG 2760

Qy 2761 ACCCTAGGGGCTGATCCTCAAGTACCCCAGTTTCACACATACCAAAACCAAGGTTCTCTCCC 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2761 ACCCTAGGGGCTGATCCTCAAGTACCCCAGTTTCACACATACCAAAACCAAGGTTCTCTCCC 2820

Qy 2821 CTCTTTCCTCTCACATACATGCTTCTGTCTCCTCTTCTTGGAATGCATGAAACTTTGATTCCT 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821 CTCTTTCCTCTCACATACATGCTTCTGTCTCCTCTTCTTGGAATGCATGAAACTTTGATTCCT 2880

Qy 2881 TCAGGCCCTTGTCAGCTACCGAAGGAAGCAGTGGCTTCACCTGTCCTTTAGGGAAG 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881 TCAGGCCCTTGTCAGCTACCGAAGGAAGCAGTGGCTTCACCTGTCCTTTAGGGAAG 2940

Qy 2941 CTGGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGCTCTGAACC 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2941 CTGGGAGCCATCTCTGCACTAACTGCCCTCCCAAATATCTTGGTTCAGACAGCTCTGAACC 3000

Qy 3001 CCACGCCTCACGTGGTCGACCTTGCCTCCCGATTTTCGGAGTTGGGGAAGGGGCCCATGACC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3001 CCACGCCTCACGTGGTCGACCTTGCCTCCCGATTTTCGGAGTTGGGGAAGGGGCCCATGACC 3060

Qy 3061 ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGGTTTCTGCCAGCTTCCCT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3061 ACCCTCGTAGACTTTTTCCATGGGATACAGTTTAGGACACGGGGTTTCTGCCAGCTTCCCT 3120

Qy 3121 AACCAGGAGGGGGGGGATGGAGAAGGGGCCTACATTTCTCAATCCAGAGGAG 3169
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db 3121 AACCAGGAGGGGGGGGATGGAGAAGGGGCCTACATTTCTCAATCCAGAGGAG 3169

RESULT 2.
US-10-487-887-3
; Sequence 3, Application US/10487887

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Db   468 TGGCACCATGCGGAGCAAGCCCTGGGCCATGGGAGAAGAGCTGACGAGCTCAGGGAGGC      527
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   576 CCAGGAATTTGTGGAGAAGTATAGAGGTGCCTGGGAAAAGGGGAAAGGCCAAGCAACTATA   635
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   528 CCAGGAATTTGTGGAGAAGTATGAAGGTGCCTGGGAAAAGGGGAAAGGCCAAGCAACTATA   587
Qy   636 TGCCCTACAAGATGCTGATGGCCAAGAAAATGGGTCAAATTTAAGAGAGACTTTGATAATTT 695
         ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   588 TGCCTACAAGATGCTGATGGCCAAGAAAATGGGTCAAATTTAAGAGAGACTTTGATAATTT   647
Qy   696 CAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGGAAGTCAACTTTGGTTC         755
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   648 CAAAGACTCAAATGTATCCCCTGGGAAATGAAGATCAAGGAAGTCAACTTTGGTTC       707
Qy   756 TTCAGTGGCATCGTATTTCATTCTTCTCCCGATGGATGTATGGAGTTAACCTTGTCCTTTT  815
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   708 TTCAGTGGCATCGTATTTCATTCTTCTCCCGATGGATGTATGGAGTTAACCTTGTCCTTTT  767
Qy   816 TGGCTTAATATTTGGTCTAGTCATAATCCCAGAGACTACTGATGGGCATGCCCTATGGGAG  875
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   768 TGGCTTAATATTTGGTCTAGTCATAATCCCAGAGACTACTGATGGGCATGCCCTATGGGAG  827
Qy   876 TATTCCCAGAAAAGAACAGTGCCTCGGGCGTGAGGAAGAAAAGGCCATGGATTTTTCTGTCCT 935
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828 TATTCCCAGAAAAGAACAGTGCCTCGGGCGTGAGGAAGAAAAGGCCATGGATTTTTCTGTCCT 887
Qy   936 TTCGGATTTTGAGGGCTATATCAAGTACTCTGCACTCTTCTTATGGGCTACTACAACAACCA  995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   888 TTCGGATTTTGAGGGCTATATCAAGTACTCTGCACTCTTCTTATGGGCTACTACAACAACCA  947
Qy   996 GAGGACCACATCGGGTGGCTGAGGTACCGGCTTACTTTATGGTGTGGGGGTCAG         1055
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   948 GAGGACCACATCGGGTGGCTGAGGTACCGGCTTACTTTATGGTGTGGGGGTCAG         1007
Qy  1056 CCGTGTTCGGCTACAGCCTACGATTATTGTCATTCGATCGGATCGGATCGGATCAGGAAG   1115
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1008 CCTGTTCGGCTACAGCCTGATTATTGTCATTCGATCGGATCGGATCGGATCAGGAAG      1067
Qy  1116 CACAGGCGGAAGGGGAGGAGTGACAACTTCACATTCAGCGTTCACCAGCTGGGA        1175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1068 CACAGGCGGAAGGGGAGGAGTGACAACTTCACATTCAGCGTTCACCAGCTGGGA        1127
Qy  1176 CTACCTGATCGGGGAATTCAGAGACGCTGATAACAAATATGCATCACATCACCACCAGCTT 1235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  1128 CTACCTGATCGGGGAATTCAGAGACGCTGATAACAAATATGCATCACATCACCACCAGCTT 1187
Qy  1236 CAAGGAATCAAATAGTGGATGAACAGAGGAGTAACAAGAGAAAATATCCATCTGACAAG    1295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1188 CAAGGAAATCAAATAGTGGATGAACAGAGGAGTAACAAGAGAAAATATCCATCTGACAAG   1247
Qy  1296 ATTTCTTCCGTCGTCTGGGCCAACTTTCTCATCACTCTGCTGTTTGTTGTGGAAGTGGGTACCT 1355
         |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1248 ATTTCTTCCGTCGTCTGGGCCAACTTTCTCATCACTCTGCTGTTTGTTGTGGAAGTGGGTACCT 1307
Qy  1356 CATTTACTTTGTGGTTAAGGGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTGGTA   1415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      [continues]                                                   1367
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Db  1308 CATTTACTTTGTGGTTAAGGGATCTCAGCAATTCTCCAAAAATGCAGAATGTCAGCTGGTA   1367
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1416 TGAAAGGAATGAGGTAGAGATCGTGATGTCCGTTGCTTGGAAATGTTTTGTCCCCTCTGTT  1475
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1368 TGAAAGGAATGAGGTAGAGATCGTGATGTCCGTTGCTTGGAAATGTTTTGTCCCCTCTGTT  1427
Qy  1476 TGAAACCATCGCTGCCCTGCCGGAGAATTACCACCCCACGCACTGGACTGAAGTGGCACTGGG 1535
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1428 TGAAACCATCGCTGCCCTGGAGAATTACCACCCCACGCACTGGACTGAAGTGGCAGGTGGG  1487
Qy  1536 ACGGATCATCTTTGCACTCTTCCTGGGGAACCTCTACACATTTCTTCTTGGGCGTGATGGGA 1595
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1488 ACGGATCATCTTTGCACTCTTCCTGGGGAACCTCTACACATTTCTTCTTGGGCGTGATGGGA 1547
Qy  1596 CGTCCACCTCAAGCTTGCTAATGAAAGCAGTAAAAAGAAACATCACTCACTGACTCTGTT  1655
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1548 CGTCCACCTCAAGCTTGCTAATGAAAGCAGTAAAAAGAAACATCACTCACTGACTCTGCC  1607
Qy  1656 TAACTATTACAACTCTTCTGGTTGGAACGAAGAGTGTCCCCGACCACCCCTGCACCCTGC   1715
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1608 TAACTATTACAACTCTTCTGGTTGGAACGAAGAGTGTCCCCGACCACCCCTGCACCCTGC   1667
Qy  1716 AGATGTGCCCCCGGGGTTCTTGCTGGGAGACAGCCTGTGGGCATTGAATTCATGAGCGTGAC 1775
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1668 AGATGTGCCCCCGGGGTTCTTGCTGGGAGACAGCCTGTGGGCATTGAATTCATGAGCGTGAC 1727
Qy  1776 GGTGTCTGACATGCTGGGTAACGTACATCACCATCCTGCTGGGGGGGGGGACTTCCTTG    1835
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1728 GGTGTCTGACATGCTGGGTAACGTACATCACCATCCTGCTGGGGGGGGGGACTTCCTTG    1787
Qy  1836 TTTTGTGCGGGTTCATGAACTACTGCTGTGGTGCTGGGACTTGGAGGCTGGGATTTCCTTCATA 1895
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1788 TTTTGTGCGGGTTCATGAACTACTGCTGTGGTGCTGGGACTTGGAGGCTGGATTTCCTTCATA 1847
Qy  1896 TGCTGAGTTTGATATTAGTGGAAATGTCTGGGTTTGATCTTCAACCAAGGAATATCTG    1955
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1848 TGCTGAGTTTGATATTAGTGGAAATGTCTGGGTTTGATCTTCAACCAAGGAATGATCTG   1907
Qy  1956 GATGGGCTCCTTCTATGCTCCAGGCGCTGGGCATTAATGTGCTGCGGCCCTGCTGACTTC   2015
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1908 GATGGGCTCCTTCTATGCTCCAGGCGCTGGGCATTAATGTGCTGCGGCCCTGCTGACTTC   1967
Qy  2016 CATGTACTTCCAGTGCTCTGGGCGGTGATGAGCAGAGCAAGTGACCCTGAACGGGGTGTTCAA 2075
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1968 CATGTACTTCCAGTGCTCTGGGCGGTGATGAGCAGAGCAAGTGACCCTGAACGGGGTGTTCAA 2027
Qy  2076 AGCCTCCCGATCCCAACAACTTCTACATGGGCCTCCTGCTGCTCTTCCTCAGCCT       2135
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2028 AGCCTCCCGATCCCAACAACTTCTACATGGGCCTCCTGCTGCTCTTCCTCAGCCT       2087
Qy  2136 CCTGCCCGGTGGCCTACACCATCACTCCCCACCCTCCTTGACTGCGGGCCCGTTCAG     2195
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2088 CCTGCCCGGTGGCCTACACCATCACTCCCCACCCTCCTTGACTGCGGGCCCGTTCAG     2147
Qy  2196 TGGGAAAAACAGAATGTACGAGTGCTCCAAGAGACCATTGAAAACGGATTTCCCAAACTT  2255
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2148 TGGGAAAAACAGAATGTACGAGTGCTCCAAGAGACCATTGAAAACGGATTTCCCAACCTT  2207
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Qy 2256 CCTGGGCAAGATCTTTGCTTTCCTTCCGCCAAATCCAGCGCCTGGATCATCCCAGCCATCCTGCT 2315
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2208 CCTGGGCAAGATCTTTGCTTTTCCTTCCGCCAAATCCAGCGCCTGATCATCCCAGCCATCCTGCT 2267

Qy 2316 GATGTTCTTGGGCCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCGGAGCTAATGC 2375
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2268 GATGTTCTTGGGCCATTTACTTACCTGAACTCAGTTTCCAAAAGCCTTTCCGGAGCTAATGC 2327

Qy 2376 CCAGCTGAGGAAGAAAAATCCAAGTGCTCCCTGAAGTTGAGAAGAGTCACAAATCTGTAAA 2435
            |||||||||
Db 2328 CCAGCTGAGGAAGAAAAATCCAAGTGCTCCCTGAAGTTGAGAAGAGTCACAAATCTGTAAA 2387

Qy 2436 AGGCAAAGCCACAGCCAGAGATTCAGAGACACACTAAAAGAGCAGCTTCAAAAAATGCCAC 2495
Db 2388 AGGCAAAGCCACAGCCAGAGATTCAGAGACACACTAAAAGAGCAGCTTCAAAAAATGCCAC 2447

Qy 2496 CCAGCTCCAACTCACCAAGGAAGAGAGACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCAT 2555
Db 2448 CCAGCTCCAACTCACCAAGGAAGAGAGACCACTCCTCCCTCTGCCAGCCAAAGCCAGGCCAT 2507

Qy 2556 GGACAAGAAGCGCCAGGCCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGC 2615
Db 2508 GGACAAGAAGCGCCAGGCCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGC 2567

Qy 2616 CTCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGACCAGATTCTGGCCACGGCCCC 2675
Db 2568 CTCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGACCAGATTCTGGCCACGGCCCC 2627

Qy 2676 ATCTCAGACTCATCCCTGGAGGTCAGCCCTCTGGAAAGAGTGCTCAGAGACCTCCCCACTG 2735
Db 2628 ATCTCAGACTCATCCCTGGAGGTCAGCCCTCTGGAAAGAGTGCTCAGAGACCTCCCCACTG 2687

Qy 2736 ACGGCTAGGACTCCAGGAGGACCTCGACCTCAGGCCTGATCCTCAAGTACCCCAGTTTCAC 2795
Db 2688 ACGGCTAGGACTCCAGGAGGACCTCGACCTCAGGCCTGATCCTCAAGTACCCCAGTTTCAC 2747

Qy 2796 ACATACCAAAACAAAGGTTCTCTCCCCCTCTTTCCTCTCACATACATGCTCTGTCTCTCTC 2855
Db 2748 ACATACCAAAACAAAGGTTCTCTCCCCCTCTTTCCTCTCACATACATGCTCTGTCTCTCTC 2807

Qy 2856 TTGGAATGCATGAACTTTGATTCCTTCAGCTACCGAAGGAGAGAAGACAG 2915
Db 2808 TTGGAATGCATGAACTTTGATTCCTTCAGCTACCGAAGGAGAGAAGACAG 2867

Qy 2916 TGGCTTCACCTGTCTTTAGGGAAGCTGGAGGCCATCTCTGCCACTAACTGCCCTCCCAAAT 2975
Db 2868 TGGCTTCACCTGTCTTTAGGGAAGCTGGAGGCCATCTCTGCCACTAACTGCCCTCCCAAAT 2927

Qy 2976 ATCTTGGTTCAGAGCAGCTCTGAACCCCAGGCTCACAGTGGTCGACCTTGCCTCCCGATTT 3035
Db 2928 ATCTTGGTTCAGAGCAGCTCTGAACCCCAGGCTCACAGTGGTCGACCTTGCCTCCCGATTT 2987

Qy 3036 TCGGAGTTGGGGAAGGGCCATGACCACACCCTCGTAGACTTTTTCCATGGGATACAGTTTAG 3095
Db 2988 TCGGAGTTGGGGAAGGGCCATGACCACACCCTCGTAGACTTTTTCCATGGGATACAGTTTAG 3047

Qy 3096 GACACGGGGTTTCTGCCAGCTTCCCTCAACCAGCAGGAGGGGGATGGAGAAGGGGCCTACATTTCT 3155
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3048 GACACGGGGTTTCTGCCAGCTTCCCTAACCAGCAGGAGGGGGGATGGAGAAGGGGCCTACATTTCT 3107

Qy 3156 CAATCCAGAGGAAG 3169
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Db 3108 CAATCCAGAGGAAG 3121

RESULT 3
US-10-450-763-28100
; Sequence 28100, Application US/10450763
; Publication No. US2005019675A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 79OCIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 28100
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1906)..(2340)
; OTHER INFORMATION: 100% homologous to Homo sapiens dJ686C3.3 (novel
; OTHER INFORMATION: gene),accession number AL049712,Smith-Waterman Score=778.
US-10-450-763-28100

Query Match   72.4%; Score 2294.6; DB 9; Length 5027;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 2545; Conservative   0; Mismatches   59; Indels 195; Gaps   2;

Qy   93 CACAGGTGACAGGCTGGGAAGGAGAGATCCTCAAGCAACAGCGGCGGCTCTCAAAGCCGAGGGGAC 152
          | |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   45 CTCAGGTGACAGGCTGGGAAGGAGGATCTCTCAAGCAGCAAGCCGGCGCTCTCAAAGCCGAGGGGAC 104

Qy 153 CCCAGGCACAGGGCCGCGAGGTCAGCGAAGCCAGGAGAGCGCGGCGCCGGCGGGCCGGCCAGCGCCC 212
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 105 CCCAGGCACAGGGCCGCGAGGTCAGCGAAGCCAGGAGAGCGCGGCGCCGGCGGGCCGGCCAGCGCC 164

Qy 213 GGGGTCTCCCCGGAGGAAGCAAACAGGGCGCGCAGGAGACACAGAGAAAGAGCTGGGGGAGCA 272
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 165 GGGGTCTCCCCGGAGGAAGCAAACAGGGCGCGCAGGAGACACAGAGAAAGAGCTGGGGGAGCA 224

Qy 273 GGAGCGGGGGCCCAGGCGAGAGAGGACCTGCGCGGCAGGAGAAAGCCCGACGAGAGGGGCCTC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 225 GGAGCGGGGGCCCAGGCGAGAGAGGACCTGCGGGCAGGAGAGAGGACGACAGGAGAAAGCCCGACGAGAGGGGCCTC 284

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Qy   333  CTTCCAGGAGGAGGCGGACAGCAGCCACCCCAAAGAGAGGGAAAAGGAGAATTCCGAGGAGGAAGGAGGAGGAA  392
          |||||| ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   285  CTTCCAGGAGGGACGCAGCCACCCCAAAGAGAGGGAAAAGGAGAATTCCGAGGAGGAAGGAGGAGGAA       344

Qy   393  GTCGAAGCGGCAGAAGAAACCAGGTCATCCTCCTTGGCCTCCAGTGCCTTCTGGTGGGGGA                452
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   345  GTCGAAGCGGCAGAAACCAGGTCATCCTCCTTGGCCTCCAGTGCCTTCTGGTGGGGGA                   404

Qy   453  GTCCCTGTCCGAGGAGGGACTGGCCCAGGATCCTGGAGCCAGGTGGAAGAAAAAGAAGCT                 512
          ||||||||||||| ||||||||||||||  |||||||||||||||||||||||||||||
Db   405  GTCCCTGTCCGAGGGGACTGGCCCCGGATCCTGGAGCCAGGTGGAAGAAAAAGAAGCT                   464

Qy   513  CATTGCCACCATGCCGGAGCAAGCCCCTGGGCCCCCCATAGGGGAGAAGCTGACCGAGCTCAGGGA          572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   465  CATTGCCACCATGCCGGAGCAAGCCCCTGGGCCGGGAGAAGCTGACAGAGAAAAAGAAGCT              524

Qy   573  GGGCCAGGAATTGTGGGAGGAGAGTATGAAGGTGCCTTGGGAAAGGGGGAAAGGCAAGCAACT            632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   525  GGGCCAGGAATTGTGGGAGGAGAGTATGAAGGCGCCTTGGGAAAGGGGGAAAGGCAAGCAACT            584

Qy   633  ATATGCCTACAAGATGCTGATGGCCCAAGAAATGGGTCAAATTTAAGAGAGACTTTGATAA             692
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   585  ATATGCCTACAAGATGCTGATGGCCCAAGAAATGGGTCAAATTTAAGAGAGACTTTGATAA             644

Qy   693  TTTCAAAGACTCAATGTATCCCCTGGGAAATGAGACATCAAGGACACATTGCACTACTTTGG            752
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   645  TTTCAAGACTCAATGTATCCCCTGGGAAATGAGACATCAAGGACACATTGAACTACTTTGG            704

Qy   753  TTCTTCAGTGGCATCGTATTCATTCTTCTCCGATGGATTGTATGGAGTTGAACCTTGTCCT            812
          ||||||    |||||||||||||||| ||||||||||||  ||||||||||||||||||||
Db   705  TTCTTCAGTGGCATCGTATTCATTCTTCTCCGATGGATTGTATGGAGTTGAACCTTGTCCT            764

Qy   813  TTTTTGGCTTAATATTTGGTCTAGTCATTAATCCCAGAGGTACT                              854
          ||||||                                     |
Db   765  TTTTTGGCTTAATATTTGGTCTAGTCATTAATCCCAGAGGTACT                              824

Qy   855  ------------GATGGGCATGCCCTATGGGGAGTGTATTCCAGAAAGA                         889
          |||   |||||||||||||||||||||||||||||||||||||||||
Db   825  ACCCTCAGTTATCGTCGCAGAGGAGCTGGCTGGCAGGCCCCCACTGGATGACAAGTTATGTA            884

Qy   890  CAGTGCCCTCGGGCTGAGGGAAGAAAAGGCCATGGATTTTTCT------------              944
          |||   |||       ||||||||||||||||||||||||||||
Db   885  CTTCTCTTCCACACATGGGATCCTTACGGTCTAGGTTTTGACCAAGGGTACAAATTATCTTGA        944

Qy   931  GGGCTGAACTGAAGAAGATCCGCTTCCAAGCTCACTCACTGGCAGATCTCAGA                     1004
          |||                                                 |
Db   945  GGGCTGAACTGAAGAAGATCCGCTTCCAAGCTCACTCACTGGCAGATCTCAGA                     1004

Qy   931  -----------                                                               930
          |||
Db   931  CTTCTCTTCCACACATGGGATCCTTACGGTCTAGGTTTTGACCAAGGGTACAAATTATCTTGA        930

Qy   931  AGATACAATTTCAAGCTTACTCACGTGGCTCTTGGCCAGGCCTCAGAAAATCTGCTTCCAA             977
          |||                        |     |  |||||||||||||||||||||||||
Db  1005  AGATACAATTTCAAGCTTACTCACGTGGCTCTTGGCCAGGCCTATATCAAGTACTCTGCACTCTCTA    1064

Qy  1065  CCTTACTTATGTGGGCTGGTCCCAAGGTTCAGGCCTATATCAAGTACTCTGCACTCTCTA           1124
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1065  CCTTACTTATGTGGGCTGGTCCCAAGGTTCAGGCCTATATCAAGTACTCTGCACTCTCTA           1124
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Qy   978  TGGCTACTACAACAACCAGGAGACCATCGGGTGGCTTGAGGTACCGGCTGCCTATGGCTTA          1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1125  TGGCTACTACAACAACCAGGAGACCATCGGGTGGCTTGAGGTACCGGCTGCCTATGGCTTA          1184

Qy  1038  CTTTATGGTGGGGTTCAGCGGTTCTGGCGTACAGCCTAGCCTGGTTGGGCTGGGCTTCATTCGATCGATTGGC  1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1185  CTTTATGGTGGGGTTCAGCGGTTCTGGGGCTACAGCCTGATTATTGTCATTCGATCGATTGGC        1244

Qy  1098  CAGCAATACCCAAGGAAGGACACAGGGGAGAAGGGGGAGGAGAGTGACAACTTCAACATTCAGCTTCAA      1157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1245  CAGCAATACCCAAGGAAGGACACAGGGGAGGAGAGTGACAACTTCAACATTCAGCTTCAA           1304

Qy  1158  GATGTTCACCAGCTGGACTACCTGATCGGGGAATTCAGAGACGAGCAGCTGATGAACAATATGCC           1217
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1305  GATGTTCACCAGCTGGACTACCTGATCGGGGAATTCAGAGACGAGCAGCTGATGAACAATATGCC           1364

Qy  1218  ATCCATCACCACCAGCTTCAAGGAATACAAATAGTGATGAATGAACAGAAGAGTAAACAAAGAGA          1277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1365  ATCCATCACCACCAGCTTCAAGGAATCAAATACTGATGAATGAACAGAAGAGTAAACAAAGAAA          1424

Qy  1278  AAATATCCATCTGACAAGATTTCTTCGTTGCTCCTGGCCAACTTTCTCATCACATCGTGTTT            1337
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1425  AAATATCCATCTGACAAGATTTCTTCGTTGCTCCTGGCCAACTTTCTCATCACATCGTGTTT            1484

Qy  1338  GTGTGGGAAGTGGGGTACCTCATTTACTTTGTTGGTTAAGGCAATCTCAGCAATTCTCCAAAAT          1397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1485  GTGTGGAAGTGGGGTACCTCATTTACTTTGTTGGTTAAGGCAATCTCAGCAATTCTCCAAAAT          1544

Qy  1398  GCAGAATGTCAGCTGGTCATGAGAGAAATGAGGTACAGATCGTGATGTCTCCTGCTTGGGAAT          1457
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1545  GCAGAATGTCAGCTGGTCATGAGAGAAATGAGGTAGGAGATCGTGATGTCCCTGCTTGGAAT         1604

Qy  1458  GTTTTGTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAATTACCACCCAGGCACTCG           1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1605  GTTTTGTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAATTACCACCCAGGCACTGG           1664

Qy  1518  ACTGAAGTGGCAGCTGGGACGGCGGCATCTTTGCACTCTTCCTGGGGGACCTCTACACATTTCT          1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1665  ACTGAAGTGGCAGCTGGGACGGCGGCATCTTTGCACTCTTCCTGGGGGACCTCTACACATTTCT          1724

Qy  1578  CTTGGCCTGACTGGATGACGTCCACCTCAAAGCTTGCTAATGAAGAGACAAATAAAGACAT           1637
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1725  CTTGGCCCTGACTGGATGACGTCCACCTCAAAGCTTGCTAATGAAGAGACAAATAAAGACAT          1784

Qy  1638  CACTCACTGGACTCTGTTTAACTATTACAACTCTTCTCGGTTGGACAGAGAGTGTCCCCG             1697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1785  CACTCACTGGACTCTGTTTAACTATTACAACTCTTCTCGGTTGGACGAGAGTGTCCCCG             1844

Qy  1698  ACCACCCCTGCACCCTGCACATGTGCCCCGGGGTTCTTGCTGGGGGACAGCTGTGGGCAT             1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1845  ACCACCCCTGCACCCTGCACATGTGCCCCGGGGTTCTTGCTGGGGGACAGCTGTGGGCAT             1904

Qy  1758  TGAATTCATGAGGCTGACGGTGTCTGACATGCTGTAGTACGTACATCACCATCCTGCTGGG            1817
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1905  TGAATTCATGAGGCTGACGGTGTCTGACATGCTGGTAAGGTACATCACCATCCTGCTGGG            1964

Qy  1818  GGACTTCCTACGGGCTTGTTTGTCGGGTTCATGAACTACTGCTGGTGCTGGGGACTTGGA           1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1965  GGACTTCCTACGGGCTTGTTTGTCGGGTTCATGAACTACTGCTGGTGCTGGGGACTTGGA           1877
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Query Match 72.4%; Score 2293; DB 6; Length 4895;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 2544; Conservative 0; Mismatches 60; Indels 195; Gaps 2;

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Qy    393 GTCGAAGCGGCGAAGAAACCAAGGTCATCCTCCTTGGCCTCCAGTGCTCTGGTGGGGA 452
          |||||| |||||| ||||||| ||||||||||||||||||||||||||||||   |||
Db    345 GTCGAAGCGGCGAGAAGAAACCCAGGTCATCCTCCTTGGCCTCCAGTGCTCTGGGGGA 404

Qy    453 GTCCCTGTCCGAGGAGGAGAAGCTCCTGGACGTCCTCCCAGATCCTGGACGTTGAAGAAGACT 512
          |||||||||||||||||||||| |||||| |||||||||||||||||||||||||||||||||
Db    405 GTCCCTGTCCGAGGAGGAGAATCCTGGACGTCCTCCCAGATCCTGGAAGAAAAAGAAGACT 464

Qy    513 CATTGCCAACCATGCGGAGCGAAGCCCTGCCCCATGGCCGAGAGAAGCTGACAGAGCTCAGGGA 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 CATTGCCACCATGCGGAGCGAAGCCCTGCCCCATGGCCGAGAGAAGCTGACAGAGCTCAGGGA 524

Qy    573 GGCCCAGGAATTTCTTGGAGAAGTAATGAAGGTGCCTCTGGGAAAGGGGAAAGGCAAGCAACT 632
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 GGCCCAGGAATTTCTTGGAGAAGTAATGAAGGTGCCTCTGGGAAAGGGGAAAGGCAAGCAACT 584

Qy    633 ATATGCCTACAAAGATGCTGATGGGCCAGAAAATGGGTCAAAATTTAAGAGAGACTTTGATAA 692
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 ATATGCCTACAAAGATGCTGATGGGCCAGAAAATGGGTCAAAATTTAAGAGAGACTTTGATAA 644

Qy    693 TTTCAAGACTCAATGTATCCCCTGGGAAAATGAAGATCAAGGACATTGAAAGTCACTTTGG 752
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    645 TTTCAAGACTCAATGTATCCCCTGGGAAAATGAAGATCAAGGACATTGAAAGTCACTTTGG 704

Qy    753 TTCTTCAGTGGCATGGTATTTCATCTTTCTCCGATGGATGTATGGGAGTTAACCTTGTCCT 812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 TTCTTCAGTGGCATGGTATTTCATCTTTCTCCGATGGATGTATGGGAGTTAACCTTGTCCT 764

Qy    813 TTTTTGGCTTAAATATTTGGTCTAGTCATAATCCCAGAGGTACT------------------ 854
          |||||||| |||     |||  |||||  |  || ||||||||
Db    765 TTTTTGGCTTAATATTTGGTCTCAGTCATAATCCCAGAGGTACT 824

Qy    855 ----GATGGGCATGCCCTATGGGAGTGTATTCCCAGAAAGA 889
              | || || || |  |||||||| ||||| ||||||||
Db    825 ACCCTCAGTTATGTCTGCAGGAGCTGGCAAGGCCCACTGGCATGACAAGTTTATGTA 884

Qy    890 CAGTGCCTCGGGGCTGAGGAGAAAAAGCCCATGGATTTTTCT----------- 930
          | ||                  ||||| ||||||||||||
Db    885 CTTCTCTTCCAACACTGGATCCTACGGTCTAGGTTTTTGACCAAGGCTACAATTATCTTGA 944

Qy    931 --------------------GTCCTTTGGGATTTTGAGGGGTATATACAGTACTCTGCACTCTTCTA 977
                              |||||  ||||||    |||| ||||
Db    931 GGCTGAACTGAAGAGAATCCGCTTCCAAGCTCACTCACATGGCTACTGGCAGATCTCAGA 1004

Qy   1005 AGATACAAATTTCAAGCTTACTCACGTGCTTCTGGCAGGCCTCAGAAAATCTGCTTCCAA 1064
          |||
Db    945 GGCTGAACTGAAGAGAATCCGCTTCCAAGCTCACTCACATGGCTACTGGCAGATCTCAGA 1004

Qy    931 --------------------- 930
Db    885 CTTCTCTTCCAACACTGGATCCTACGGTCTAGGTTTTTGACCAAGGCTACAATTATCTTGA 944

Db   1065 CCTTACTTATGTGCTTACTCAAGGTTCAGGGCTATATCAAGTACTCTGCACTCTCTA 1124

Qy    978 TGGCTACTACAACAACCAGAGGACCATCGGGGTGGCTGAGGTACCGGGCTGCCTAGGCTTA 1037
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1125 TGGCTACTACAACAACCAGAGGACCATCGGGGTGGCTGAGGTACCGGGCTGCCTAGGCTTA 1184

Qy   1038 CTTTATGGTGGGGGTCAGCGGTGTTCGGCCTACAGCGCTGATTATTGTCATTCGATCGATGGC 1097
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1185 CTTTATGGTGGGGGTCAGCGGTGTTCGGCCTACAGCGCTGATTATTGTCATTCGATCGATGGC 1244

Db   1098 CAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGAGTGACAACTTCACATTCAGCTTCA 1157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1245 CAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGAGTGACAACTTCACATTCAGCTTCA 1304

Db   1158 GATGTTCACCACCTGGGACTACCTGATCCGGGAATTCAGAGACAGCTGATAACAAATATGC 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1305 GATGTTCACCACCTGGGACTACCTGATCCGGGAATTCAGAGACAGCTGATAACAAATATGC 1364

Db   1218 ATCCATCACCACCAGCTTCAAGGAATCAATCAATAGTGGATGAACAAGAAGAGTAACAAAGAAGA 1277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1365 ATCCATCACCACCAGCTTCAAGGAATCAATCAATAGTGGATGAACAAGAAGAGTAACAAAGAAGA 1424

Db   1278 AAATATCCATCGACAAGATTCTTCGTCGTCCTGGCCACACTTTCTCATCATCTGCTGTTT 1337
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1425 AAATATCCATCTGACAAGATTCTTCGTCGTCCTGGCCAACTTTCTCATCATCTGCTGTTT 1484

Db   1338 GTGTGGAAGTGGGCTACCTCATTTACTTTGTGGTTAAGCCGATCTCACGAATTCTCCAAAAT 1397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1485 GTGTGGAAGTGGGGTACCTCATTTACTTTGTGGTTAAGCCGATCTCACGAATTCTCCAAAAT 1544

Db   1398 GCAGAAGTGTCACCTGGTATGAAAGGAATGAGTACAGAGATCGGTGATGTCCCTGCTTGGAAT 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1545 GCAGAAGTGTCACCTGGTATGAAAGGAATGAGTACAGAGATCGGTGATGTCCCTGCTTGGAAT 1604

Db   1458 GTTTTGTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAATTACCACCACCAGCACTGG 1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1605 GTTTTGTCCCCCTCTGTTTGAAACCATCGGCTGCCCTGGAGAATTACCACCACCAGCACTGG 1664

Db   1518 ACTGAAGTGGCAGCTGGGACGGAGGCGATCTTTGCACTCTTCCTGGGGAACCCTCTACACATTTCT 1577
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1665 ACTGAAGTGGCAGCTGGGACGGAGGCGATCTTTGCACTCTTCCTGGGGAACCCTCTACACATTTCT 1724

Db   1578 CTTGGCCCTGATGGATGACGGTCCACCTCAAGCTTGCTAATGAAGAGACAAATAAAGAAACAT 1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1725 CTTGGCCCTGATGGATGACGGTCCACCTCAAGCTTGCTAATGAAGAGACAAATAAAGAAACAT 1784

Db   1638 CACTCACTGGACTCTGTTTAACTATTACAACTCTTCTGGTTGGAACGGAGAGTGTCCCCG 1697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1785 CACTCACTGGACTCTGTTTAACTATTACAACTCTTCTGGTTGGAACGGAGAGTGTCCCCG 1844

Db   1698 ACCACCCCTGCACCTGCGACGATGTGCCCCGGGGTTCTTCCTCGTGACAGCTGGGGCAT 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1845 ACCACCCCTGCACCTGCGACGATGTGCCCCGGGGTTCTTCCTCGTGACAGCTGGGGCAT 1904

Db   1758 TGAATTCATGAGGCTGACCTGGTGCTCTGACATGCTGGTAACGGTACACTACCATCCTGCTGG 1817
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1905 TGAATTCATGAGGCTGACCTGGTGCTCTGACATGCTGGTAACGGTACACTACCATCCTGCTGGG 1964

Db   1818 GGACTTCCTACGGGGCTTGTTTGTGCGGGTTCATGAAACTACTACGTGCTGGTGCTGGGGACTTGGA 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1965 GGACTTCCTACGGGGCTTGTTTGTGCGGGTTCATGAAACTACTACGTGCTGGTGCTGGGGACTTGGA 2024

Db   1878 GGCTGGATTCCTTCATATGCTGAGTTTGATATTAGTGAAAATGCTCGGGTTTGATCTT 1937
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     -- GGCTGGATTCCTTCATATGCTGAGTTTGATATTAGTGAAAATGCTCGGGTTTGATCTT 1937
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Db   2025  GGCTGGATTTCCTTCATATGCTGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATCTT   2084

Qy   1938  CAACCAAGGAATGATCTGGATGGGCTCCTTCTTATGCTCCCAGGCCTGGTGGGCATTAATGT   1997
           ||||||
Db   2085  CAACCAAGGAATGATCTGGATGGGCTCCTTCTTATGCTCCCAGGCCTGGTGGGCATTAATGT   2144

Qy   1998  GCTGCGCCCTGCTGACCTCCATGTACTTCCAGTGTGCTGGGCGGTGATGACCAACGTACC   2057
           |||||||
Db   2145  GCTGCGCCCTGCTGACCTCCATGTACTTCCAGTGTGCTGGGCGGTGATGACCAACGTACC   2204

Qy   2058  CCATGAACGGCGGTCGTTCAAAGCCTCCCGATCCAACACACTTCTACATGGGCCTTCCTTGCTGCT   2117
Db   2205  CCATGAACGGCGGTGTTCAAAGCCTCCCGATCCAACACTTCTACATGGGCCTTCCTTGCTGCT   2264

Qy   2118  GGTGCTTCTTCCTCAGCCTCCTGCCGGTGGGCCTACAGCACCATCATGTCCCTCCCACCCTCCTT   2177
Db   2265  GGTGCTTCTTCCTCAGCCTCCTGCCGGTGGGCCTACAGCACCATCATGTCCCTCCCACCCTCCTT   2324

Qy   2178  TGACTGCGGGGCGGTTCAGTGGGGAAAAACAGAATGTACGATGTCCTCTCCCAAGAGACCATTGA   2237
Db   2325  TGACTGCGGGGCGGTTCAGTGGGGAAAAACAGAATGTACGATGTCCTCCAAGAGACCATTGA   2384

Qy   2238  AAACGATTTCCCAAACTTCCTGGGCAAGATCTTTGCTTTCCTCGCCAATCCAGGCCTGAT   2297
Db   2385  AAACGATTTCCCAAACTTCCTGGGCAAGATCTTTGCTTTCCTCGCCAATCCAGGCCTGAT   2444

Qy   2298  CATCCCAGCCATCCTGCTGATGTTCTTGGGCCATTTACTTACCTGAACTCAGTTTCCAAAAG   2357
Db   2445  CATCCCAGCCATCCTGCTGATGTTCTTGGGCCATTTACTTACCTGAACTCAGTTTCCAAAAG   2504

Qy   2358  CCTTTCCCGAGCTAATGCCCAGCTGAGGAGAGAAAATCCCAGTGCTGCTCCGTGAAGTTGAGA   2417
Db   2505  CCTTTCCCGAGCTAATGCCCAGCTGAGGAGAAGAAAATCCCAGTGCTGCTCCGTGAAGTTGAGA   2564

Qy   2418  GAGTCACAAAATCTGTAAAAGGCAAAGCCACAGCCAGCCGAGACACACCTAAAG   2477
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Qy   2538  CAGCCAAAGCCAGGCCATGGACAAGAGAGGCCCAGGCCCTGGGAGACCTCCAATTCTGCCAG   2597
Db   2685  CAGCCAAAGCCAGGCCATGGACAAGAGAGGGCCAGGCCCTGGGACCTCCAATTCTGCCAG   2744

Qy   2598  CAGGACCACACTCGCCTGCCTCTGGACACCTTCCTTATATCTCGGCCCCCCTGGAATCGGACC   2657
Db   2745  CAGGACCACACTGCCTGCCTCTGGACACCTTCTATATCTCGGCCCCCCTGGAATCGGACC   2804

Qy   2658  AGATTCTGGCCCACGCCCCATCTCAGACTCATCCGTGGAG   2696
Db   2805  AGATTCTGGCCCACGCCCCATCTCAGACTCATCCGTGGAG   2843
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; Sequence 7, Application US/10487887
; Publication No. US20040249139A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 7
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-487-887-7

Query Match 61.8%; Score 1957.6; DB 8; Length 3216;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 2241; Conservative 0; Mismatches 429; Indels 6; Gaps 2;

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Qy     96  AGGTGACAGGCTGGGAAGGAGGAGGATCCTCAAGCAAGCGCGGGCTCTCAAAGCCGAGGGGACCCC    155
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Db    354  AGGTGACAAGTCAGCAAGGAGACCCACAAGGAAACAAACCTCCAGAGCTGCATGTCCCCA    413

Qy    156  AGGCACAGGCCGGAGCTCACGGAAGCCAGAAGGAGGCCGGAAGCCGGGGGAGCCAAGCCCGGG    215
           || |  ||||    ||  ||    ||  || ||    |  ||  ||  ||  |    ||||
Db    414  AGACGGGCACCGAGCCCAATCTAGCCGGAAGGATCCTGCTAAGGGTAGCCCAAGACCAGG    473

Qy    216  GTCTCCCCGGAGGAAGGAGAAAACAGGCGGCGAGGAGGACACAGAGAAGAGAGCTGGGGGCAGGAGGA    275
           |||| ||||| || |||  |   |  |   |  ||  |    |||||  ||  ||    |     |||
Db    474  GTCTTCCCGGAAGGAAACAGATGGAAGCATGGAAGCTATCACAAGGGGTTGCAGGGACAGAA    533

Qy    276  GCCGGGGCGAGGCAGGAGGAGGGACCTGCGAGGGCAGGAGAAAGGCCGACGACGAGAGGGCCTCCTT    335
           |  |   |  ||  |||    |||     ||    ||||  |||  |  |   |  |||    |||
Db    534  ACCACGAAAGGTGGAGAGGTCTCTACAGCGGGGAGGGAGGAAGAG---GACCGGAGAAACTTCCCT    590

Qy    336  CCAGGAGCGGAGCAGCAGCGCCCCAAAGAGGGGAAAAGGGGAGGATTCCGAGGAGGAGGAGAGTC    395
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Db    591  TAAGGAGCAGAGAGCAATCTCCAAAGAAGGAGGAGGGGCTCTGAGGAGGAGG---CAGG    647

Qy    396  GAAGGGGCAGAGAAGAAACCCAGGTCATCCTCCTTTGGCCTCCCAGTGCCTCTCGGTGGGGAGTC    455
           ||| |  | || ||||||||||||||  |  |||||||||||| ||||  |||   |||  ||||
Db    648  CAAGCAGCTGAGAAAACCCAGGTCCACTTCCTTGGGCCTCCAGTGTCTCTACTGGAGACTC    707

Qy    456  CCTGTCCGAGGAGGAGGAACTGGCCCCAGATCCTGGAGCAGGTTGGAAGAAGAAAAGAAGAGAAGGCTCAT    515
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Qy   516 TGCCACCATCGCGGAGCAAGCCCTCGGCCCATCGGCCATGGCAGAAGAGCTGACGAGCTCAGGAGGC 575
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Db   768 CACTACCGCTGAGGAGAAACCCTGGGCCCATCGGCAAAGGAACTGAGGGAACTCAGGGAAGC 827

Qy   576 CCAGGAATTTGTTGGAGAAGTATGAAAGGTTGCCTTGGGAAAGGGGAAAGGCAAGCAAACTGGAAGC 635
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Qy   636 TGGCTACAAGATGCTGATCGGCCAAGAAATGGGTCAAATTTAAGAGAGACTTTGATAATTT 695
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Db   888 CGCCTACAGGATGATGATGGCTAAGAAAATGGGTCAGTTTAAGAGGGACTTTGATAATTT 947

Qy   696 CAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGGACATTCACTTTGGTTC 755
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Db   948 CAAGACTCAATGTATTCCCTGGGAAATGAAGATCAAGGACATTGAAAAGTCACTTCGGTTC 1007

Qy   756 TTCAGTGGCATCGTATTTCATCTTTCTCCCATGGATGTATGGGAGTTAACTTGTTCCTTTT 815
         |||| ||||||| |||| || | |||| ||||||| |||| || ||| |||||||||
Db 1008 TTCTGTGGCATCTTACTTCATCTTTCTCCGATGGGATTGGAGTTAACCTTGTCCTTTT 1067

Qy   816 TGGCTTAAATATTTGGGTCTAGTCATAATCCCAGAGGTACTGATGGGATGCCCTATGGGAG 875
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Db 1068 TGGCTTAAATATTTGGGTCTAGTCATCATCCCAGAGAGTGCTGATGGGCACGCCCTATGGAAG 1127

Qy   876 TATTCCCAGAAAGACAGTGCCTCCGGGCTGAGGAAGAAAAGGCCATGGAGATTTTTCTGTTCCT 935
         ||| |||| | | ||| |||| ||| |||||| | ||| ||||||| || | || ||
Db 1128 TATACCCAGAAAGAACCGGTGCCTCGAGCTGAGGAAGAAGCGAGCCCATGAACTTCTCGTCCT 1187

Qy   936 TTGGGATTTTGAGGGCTACATCAAAATATTCTGCTCCTTTCTATGGCTACTACAACACCA 995
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Db 1188 TTCGGAATTGTTGAGGGCTTATATCAAGTACTCTGCGACTCTTCTTATGGGCTACTACAACACCA 1247

Qy   996 GAGGACCACTCGGGGTGGCTGAGGTACCGGGCTGCCTATGGCTTACTTAATGGTGGGGGTCAG 1055
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Db 1248 GCGGACCATTGGATGGCTGAGGTACAGGGCTGCCCATGGCTTACTTAATGGTGGGGGTCAG 1307

Qy 1056 CGTGTTCGGCTCACAGCCTGATTATTGTCATTCGGATCGGATGGCCAGCAAATACCAAGGGAG 1115
         |||||| |||| ||| || || || ||||| |||| | ||||| ||| ||| ||||||||
Db 1308 CGTGTTGGCTCACAGCTTGATGATCGTCATTAGGTCGATGGCCAGCAAATACCAGGGTAG 1367

Qy 1116 CACAGGCGAAGGGGAGAGTGCAGAACTTCACATTCACATCTGTTGTTCACCAGCTGGGA 1175
         |||| || ||||| ||||||||||||||||| ||| || ||||| || ||||||||||
Db 1368 CACCAGTGAGGGGGACGAGTGACAGCTTCACATTGCATTGTCATGTTCACCAGCTGGGA 1427

Qy 1176 CTACCTGATCGGGGAATTCAGAGACACAGCAGATACAAATAATGCATCCATCACCACCAGCTT 1235
         ||||| ||||||||||||| || || |||| || |||| ||| |||||||| |||||||
Db 1428 CTACTCATCGGGGAATTCAGAGACAGCAGCAGACACAAATAATGTTCCATCACTACCAGCTT 1487

Qy 1236 CAAGGAAATCAATAGTGGTGATGAACAAGAGTAACAGAAAAAATAATCCATTCTGACAAG 1295
         || || || | ||||| ||||||||| ||||||| ||||| || |||| | || ||
Db 1488 CAAGGAGTTCTATAGTGGATGGACAACAGAGGTAACAGAAATATTCACCTGACAAG 1547

Qy 1296 ATTTCTTCGTTGTCCTGGCCAAACTTTCTCATCATCATCTGTTTGTTGTGGGAAGTGGGTACCT 1355
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Db 1548 ATTCCTCCCGCGTCCGCGGCCAACTTTCTTCATTCTCTGCTGTCTGTGTGGGAACGGGGTACCT 1607

Qy 1356 CATTTACTTTGTTGGTTAAGCGGATCTCAGCAAATTCTCCAAAATGCAGAATGTTCAGCTGGTA 1415
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Db 1608 CATTTACTTTGTGGGTTAAGCGGTTCCCAGGAGTTCTCCAAAAATGCAGCTTGGTA 1667

Db 1416 TGAAAGGAATGAGGTAGAGATCGTGATCGTCCCTGCTTGGAAATGTTTTGTCCCCTGCTTGTT 1475
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Qy 1668 TGAAAGGAATGAGGGGAGATCGTGATGTCTTCTTTGGCTAGGGATGTTTGTCGCCCCTGCTT 1727

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Qy 1728 TGAAACACCGCTGCCTTGGAGAATTATCACCCACACCAAACTGGGCTGAAGTGGGCAGCTGGG 1787

Db 1536 ACCCATCTTTGCACTCTTCCTGGGAGAACCTTCTACACATTTCTCTTGGCCCTGATGGATGA 1595
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Qy 1788 CCCGCATCTTTGCCCTCTTCCTGGGAAAACCTCTACACAGTTTCTCCTGGCCCCTCATGGACGA 1847

Db 1596 CGTCACCTCAGCTTGCTAATGAACAGCAATAAAGACACTCACTCACTGACACTCTGTT 1655
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Qy 1848 TGTCCACCTTAAGCTTCTTAATGAGGAAAAAACATCAACATCACTCACTGGACCCTGTT 1907

Db 1656 TAACTATTACAACTCTCTTCTGGGTTGAAAGGAGTGTCCCCGGACCACCCCTGACCCTGC 1715
         ||| |||| |||| | || ||||| | ||||||||| |||||||| || |||||||||
Qy 1908 TAACTATTACAATTCCTCAGTGGGAAATGAGAGTGTGCCCGGGCCACCACACCCTGC 1967

Db 1716 AGATGTGCCCCGGGGGTTCTTGCTGGGAGGAGACAGCTGTGGGGCCATTGAATTCATGAGGGTGAC 1775
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Qy 1968 AGATGTGCCCAGGAGGTTCTTGCTGGGGGAGACAGCTGTGGGGCCATTGAGTTTATGAGGGCTCAC 2027

Db 1776 GGTGTCTGACATGCTGGTAACGTACATCACCATCTCCTGCTGGGGGGACTTCCTGACCTGG 1835
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Qy 2028 CGTGTCTGACATGCTGGTAACATACATCACTATCTGGTCCGGAGATTCCTCCGGACCTTG 2087

Db 1836 TTTTGTCGCGGTTCATGAACTACTACTGGTCTGTTGTGGGGACTTGGAGGCTGGAATTCTTCATA 1895
         ||||| |||| ||||||||||| |||| |||| |||| | ||||| | | | |||||||||||
Qy 2088 TTTTGTCCGGTCATGGAATCACTGCTGGTCTGTGGGGACTTGGGGGCTGGGTTTTCCCCATA 2147

Db 1896 TGCCTGAGTTTGATTAGTTAGTGGAAAATGTGCTGGGTTTGATCTTCAACCAAGGAAATGATCTG 1955
         |||||||| ||||| | || |||| | |||| ||||| ||| || |||||| | ||||| |||
Qy 2148 TCCCAGGTTTGATTATTAGTGGAAATGTTTGGGTTTGATCTCACCAAGGAAATGATCTG 2207

Db 1956 GATGGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCCATTAATGTGCTGCCGCCTGCTGACCTC 2015
         ||||| || | | ||| |||| || || ||||| || | ||| | | ||| || || |||
Qy 2208 GATGGGGGCTTCTATGCTCCAAGGACTGGTGGGCATCAATGTCCTGCCCTGTTGACCTC 2267

Db 2016 CATGTACTTCAGTGCTGGGGCGGGTGATGGAGCAGCACAAGCTACCCCACTGATGAACGGCGTTGACA 2075
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Qy 2268 CATGTACTTCCAGTGCTGGGGCAGTGATGGAGCAGCACAAGCTGCCCCACGAGTTGTTTAA 2327

Db 2076 AGCCTCCCGATCCAACAACTTCTTACATGGGCCCTTCTGCTTCCTTCCTCAGCCT 2135
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Qy 2328 AGCCTCCAGATCCAACAACTTCTTACATGGGCCCTGCTTGCTTCCTTCCTCAGCCT 2387

Qy 2136 CCTGCGCGTGGCCTACCATCATGTGCCTCCCACCCTCCTTGACTGGGGCCGGGTTCAG 2195
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Db 2388 CCTGCCTGTGGCCTACACGGTCATGTGTCTCCCACACCTGCTTGACTGTTGGCCCCTTCAG 2447

Qy 2196 TGGGAAAAACAGAATGTACGAATGTCCTCCAAGAGACCATTGAAAAACGATTTCCCAAACTT 2255
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Db

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Db  2448  TGGGAAAAAACAGAAATGTACGATGTGCCTCCAATGAGACCATCGAAGACGATTTCCCTAAGTT  2507
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Qy  2256  CCTGGGCCAAGATCTTTGCTTTCCTGCCCAATCCAGGGCCTGATCATCCCAGCCATCCTGCT  2315

Db  2508  CCTGGGCCAAGATCTTTGCGTTCCTTGCCCACCAGGGCCTGATCATTCCAGCCATCCTGCT  2567
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Qy  2316  GATGTTCTTGGCCATTTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGGTAATGC  2375

Db  2568  AATGTTTCTGGCCATTTACTATCTGAACTCAGTTTCAAAAGTCTTTCTAGAGGTAATGC  2627
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Qy  2376  CCAGCTGAGGAAGAGAAAAATCCAATGTGCTCCGTGAAGTTGAGAAAGTCACAAATCTGTAAA  2435

Db  2628  CCAGCTGCGAAAGAAGATCCAAGCGGCTCCCGTGAAGTTGAGAAGAACCATAAATCCATCAA  2687
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Qy  2436  AGGCAAAGCCCACAGCCAGAGATTCAGGAGACACAACCTAAAAGCAGCTCCAAAAATGCCAC  2495

Db  2688  GGGAAAAAGCCATAGTCACATATTCAGAGGACACAATCAACAAGCAGCTCCAAAAATGCCAC  2747
             || |||| |||| | |||||||||||||||||| ||| |||||||||||||||||||||||
Qy  2496  CCAGCTCCAACTCACCAAGCAAGAAGAGAGACCACTCTCCCTCTCCCAGCCAAAGCCAGGGCAT  2555

Db  2748  CCAGATACATCTTACTAAAGAGAGCCCCACTCCAGTACTCAGTACTGAGGGGGGCCTGCCCATCTAC  2807
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Db  2808  GGACAAGAAAGCCCAGGGCCCCACCACCTCCAGTACTGAGGGTGGGGCCTCGGCCATCTAC  2867
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Qy  2616  CTCTGGACACACTTCCTATATATCTCGGGCCCCCTGGAATCGGACCAGATTCTGGCCACGCGCCC  2675

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Qy  2676  ATCTCAGACTCATCCGTGGAGGTCAGGCCTCTGGAAAGGAGTGCTCAGAGACCTCCCACTG  2735

Db  2928  GTCTCAGACTTACACAGGCAGGTCACCTTCTGGAAAGAGAGAACCCAGAGGGCCTCACAACTG  2987
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Qy  2736  ACGGCTAGGACTCCAGGGAGGCCTCGACCCTAGGGCT  2771

Db  2988  ATTTTCTGGCGATTCATGGGTGTCCCAGTCCTTGGCT  3023
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 06:28:46 ; Search time 254 Seconds
                (without alignments)
                3881.591 Million cell updates/sec

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgctgaccatgag..........atttctcaatccagaggaag 3169

Searched: 3289866 seqs, 15557593 residues

Total number of hits satisfying chosen parameters: 6797732

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   Published Applications NA_New:*
    1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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SUMMARIES

Result No.		Score	% Query Match Length	DB	ID	Description
c	1	106.8	3.4	1559	6	US-10-750-185-45753	Sequence 45753, A
c	2	104.6	3.3	1177	6	US-11-102-240-1129	Sequence 129, App
c	3	62	2.0	1611	6	US-10-750-185-52663	Sequence 52663, A
c	4	42.8	1.4	774	6	US-10-750-185-36837	Sequence 36837, A
c	5	42.2	1.3	2201	6	US-10-821-234-91	Sequence 91, Appl
	6	40	1.3	2031	7	US-11-135-855-5	Sequence 5, Appli
	7	40	1.3	2154	7	US-11-135-855-6	Sequence 6, Appli
	8	39.8	1.3	1280	6	US-10-750-185-32786	Sequence 32786, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Search completed: November 30, 2005, 13:27:54
Job time : 2233 secs

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2005, 04:49:06 ; Search time 11159 Seconds
                 (without alignments)
                 13286.877 Million cell updates/sec

Title: US-10-792-307-3
Perfect score: 3169
Sequence: 1 gcagtgctgaccatgag.........atttctcaatccagaoggaag 3169

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	606.4	19.1	1827	10	AY406224	AY406224 Homo sapi
2	452.8	14.3	1827	10	AY406226	AY406226 Mus muscu
3	435	13.7	11482	4	HSM806678	BX640632 Homo sapi
4	362.4	11.4	740	5	BU262560	BU262560 Homo sapi
5	327.6	10.3	450	3	BM482906	BM482906 535995 NA
6	274	8.6	595	11	DQ031957	DQ031957 Homo sapi
7	274	8.6	1656	4	AK016832	AK016832 Mus muscu

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o  9   39.6  1.2  5468    6  US-10-821-234-49       Sequence 49, Appl
   10  38.8  1.2  1600    6  US-10-750-185-57179    Sequence 57179, A
o  11  38.6  1.2  1211    6  US-10-750-185-51604    Sequence 51604, A
o  12  38.6  1.2  3301    6  US-10-750-185-42771    Sequence 42771, A
   13  37.8  1.2  207908  7  US-11-112-908-21       Sequence 21, Appl
   14  37.8  1.2  212805  7  US-11-112-908-19       Sequence 19, Appl
   15  37.6  1.2  1670    6  US-10-131-826A-325     Sequence 325, App
   16  37.6  1.2  155515  7  US-11-112-908-42       Sequence 42, Appl
   17  37.6  1.2  159660  7  US-11-112-908-43       Sequence 43, Appl
o  18  37    1.2  2952    6  US-10-689-742-211      Sequence 211, App
   19  36.8  1.2  3122    6  US-10-750-185-38196    Sequence 38196, A
   20  36.8  1.2  188682  7  US-11-112-908-23       Sequence 23, Appl
   21  36.6  1.2  1932    7  US-11-137-465-21       Sequence 21, Appl
   22  36.6  1.2  1962    7  US-11-137-465-22       Sequence 22, Appl
o  23  36.6  1.2  166111  7  US-11-112-908-47       Sequence 47, Appl
   24  36.2  1.1  686     6  US-10-750-185-25619    Sequence 25619, A
   25  36.2  1.1  1278    6  US-10-750-185-45421    Sequence 45421, A
   26  35.8  1.1  722     6  US-10-750-185-52473    Sequence 52473, A
   27  35.4  1.1  636     6  US-10-821-234-615      Sequence 615, App
   28  35.4  1.1  2376    7  US-11-056-621-3        Sequence 3, Appli
o  29  35.2  1.1  1300    6  US-10-750-185-35427    Sequence 35427, A
o  30  35.2  1.1  1412    6  US-10-821-234-266      Sequence 266, App
o  31  35.2  1.1  1893    6  US-10-750-185-35288    Sequence 35288, A
   32  34.8  1.1  3671    6  US-10-131-826A-141     Sequence 141, App
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o  38  34.4  1.1  188682  7  US-11-112-908-23       Sequence 23, Appl
o  39  34.2  1.1  767     6  US-10-750-185-26125    Sequence 26125, A
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Search completed: November 30, 2005, 13:32:10
Job time : 257 secs

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KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 1827)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
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  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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 13   244.2  7.7   822  11   DQ030264   DQ030264 Homo sapi
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ORIGIN

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Matches 607;  Conservative  0;  Mismatches 1141;  Indels  0;  Gaps  0;

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Qy   1949  TGATCTGGATGGGCTCCTTCTATGCTCCAGCGCCTGGTGGGCATTAATGTGCTGCGGCCCTGC  2008
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 21:28:08 ; Search time 10016 Seconds
                  (without alignments)
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Title: US-10-792-307-4
Perfect score: 906
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Scoring table: OLIGO
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Searched: 5883141 seqs, 2842172653 residues

Word size: 70

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
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Database :   GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	198	21.9	2560	8	AX833218	AX833218 Sequence
3	198	21.9	2560	8	AK094789	AK094789 Homo sapi
4	102	11.3	3566	6	CQ850588	CQ850588 Sequence
5	102	11.3	3566	8	AK127751	AK127751 Homo sapi
6	99	10.9	884	8	CQ728483	CQ728483 Sequence
7	99	10.9	3216	9	AF417581	AF417581 Mus muscu
8	95	10.5	159272	8	HSDJ686C3	AL049712 Human DNA
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ALIGNMENTS

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VERSION   AF417580.2 GI:28642834
KEYWORDS   .
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REFERENCE   1 (bases 1 to 3169)
  AUTHORS   Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
            Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
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            Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
  TITLE   Dominant and recessive deafness caused by mutations of a novel
            gene, TMC1, required for cochlear hair-cell function
  JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
  PUBMED   11850618
REFERENCE   2 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
REFERENCE   3 (bases 1 to 3169)

AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE   Direct Submission
JOURNAL   Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
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REMARK   Sequence update by submitter
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US-10-792-307-4 (1-906) x AF417580 (1-3169)

Alignment Scores:

Pred. No.:

Score: 0   Length: 3169
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Query Match: 100.00% Mismatches: 0
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Qy 101 ArgAspGluArgAlaSerPheGlnGluArgThrAlaAlaProLysArgGluLysGluIle 120
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Qy 121 ProArgLysGluGluLysSerLysArgGlnLysProArgSerSerSerLeuAlaSer 140
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Qy 141 SerAlaSerGlyGlyGluSerLeuSerGluGluGluLeuAlaGlnThrLeuGluGlnVal 160
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Db 436 AGTGCCTCTGGTGGGGAGTCCCTGTCCGAGGAGGAACTGGCCCAGACTCTGGAGCAGGTG 495

Qy 161 GluGluLysLysLeuLeuIleAlaThrMetArgSerLysProTrpProMetAlaLysLys 180
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Qy 181 LeuThrGluLeuArgGluAlaGlnGluValGluValLysTyrGluAlaGlyAlaLeuGlyLys 200
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Db 616 GGGAAAGGCAAGCAACTATATCCTACAGAGATGCTGATGGCAAAGAAATGGGTCAAATTT 675

Qy 221 LysArgAspPheAspAsnPheLysThrGlnCysIleProTrpGluMetLysIleLysAsp 240
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Db 676 AAGAGAGACTTTGATAATTCAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGGAC 735

Qy 241 IleGluSerHisPheGlySerValAlaSerTyrPheIlePheLeuArgTrpMetTyr 260
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Db 736 ATTGAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATTCTTCTCCGGTGGATGTAT 795

Qy 261 GlyValAsnLeuValLeuPheGlyLeuLeuPheGluValIleIleIleProGluValLeu 280
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Qy 281 MetGlyMetProTyrGlySerIleProArgLysThrValProArgAlaGluGluGluLys 300
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Qy 301 AlaMetAspPheSerValLeuTrpAspPheGluGlyValIleLysTyrSerAlaLeuPhe 320
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Db 916 GCCATGGGATTTTCTGTCCTTTGGGATTTTGAGGGCTATATCAAGTACTCTGCACTCTTC 975

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Db  976 TATGGCTACTACAACAACCAGAGGACCATCGGGTGGCTGCGCTACCGCCTATGGCT 1035

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Qy  361 AlaSerAsnThrGlnGlySerThrGlyGlyGluGlyGluSerAspAsnPheThrPheSerPhe 380
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Qy  401 AlaSerIleThrPheSerPheLysGluSerIleValValAspGluGlnLeuSerAsnLysGlu 420
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Db 1276 GAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGT 1335

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Qy  481 MetPheCysProProLeuPheGluThrIleAlaLeuGluAsnTyrHisProArgThr 500
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Qy  621 GluAlaGlyTyrPheProSerTyrAlaGluPheAspIleSerGlyLysAsnValLeuLeuIle 640
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Qy  641 PheAsnGlnIleMetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsn 660
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Qy  681 ProHisGluArgValProPheLysAlaSerArgAsnAsnPheTyrMetGlyLeuLeu 700
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Db 2056 CCCCATGAACGGGTGCCGTTCAAAGCCTCCAGAAACAACTTCTACATGGGCCTCCTG 2115

Qy  701 LeuValLeuPheLeuSerLeuLeuProValAlaLeuPheLeuAlaPheLeuAlaAsnProGlyLeu 720
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Qy  721 PheAspCysGlyProPheSerGlyLysLysAsnArgMetTyrAspValLeuGlnGluThrIle 740
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Db 2236 GAAAACGATTTCCCAAACCTTCCTGGGCAAGATCTTTGCTTTCCTCGCCAAATCCAGGCCTG 2295

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Db 2296 ATCATCCCAGCCATCCTGCTGATGTTCCTTGCCATTACTACCTGAACTCAGTTTCCAAA 2355

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Qy  801 LysSerHisLysSerValLysGlyLysAlaThrAlaArgAspSerGluAspThrProLys 820
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Db 2596 AGCAGGACCACACTGCCTGCCTCTGGACACCTTCCTATATCTCGGGCCCCCTGGAATCGGA 2655

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Db   2656 CCAGAATTCTGCCACGGCCCCATCTCAGACTCATCCGTGGAGGTCAGCCTCTGGAAAGAGT 2715

Qy   901 AlaGlnAsnArgProProHis 906
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RESULT 2
AX833218
LOCUS   AX833218   2560 bp   DNA   linear   PAT 15-DEC-2003
DEFINITION Sequence 342 from Patent EP1347046.
ACCESSION   AX833218
VERSION   AX833218.1 GI:39919353
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE   Full-length cDNA sequences
  JOURNAL   Patent: EP 1347046-A 342 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES   Location/Qualifiers
     source   1..2560
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ORIGIN

US-10-792-307-4 (1-906) x AX833218 (1-2560)

Alignment Scores:
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Percent Similarity: 100.00%   Conservative: 0
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Qy 447 LeuIleTyrPheValValLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrp 466
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Qy 467 TyrGluArgAsnGluValGlyIleValMetSerLeuLeuGlyMetPheCysProProLeu 486
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Qy 487 PheGluThrIleAlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeu 506
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Db 182 TTTGAAACCATCGCTCTGGAGAATTACCACCCACGCACGGGACTGGAAGTGGCAGCTG 241

Qy 507 GlyAlaArgIlePheAlaLeuPheLeuGlyAsnLeuThrTyrPheLeuLeuAlaLeuMetAsp 526
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Qy 527 AspValHisLeuLysLeuAlaAsnGluGluThrIleLysAsnIleThrHisTrpThrLeu 546
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Qy 567 AlaAspValProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeu 586
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Db 482 ACGGTGTCCGACATGCTGGTAACGTACATCACCATCCTGCTGGGGAAGTTCCTACGGGCT 541

Qy 607 CysPheValArgPheMetAsnTyrCysTrpCysTrpAspAspLeuGluValAlaGlyPhe 624
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RESULT 3
AK094789
LOCUS   AK094789   2560 bp   mRNA   linear   PRI 30-JAN-2004
DEFINITION Homo sapiens cDNA FLJ37470 fis, clone BRAWH2012258.
ACCESSION   AK094789
VERSION   AK094789.1 GI:21753918
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,
            Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
            Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
            Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,
            Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,
            Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,
            Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,
            Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,
            Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,
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            Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R.,
            Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A.,
            Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T.,
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            Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,
            Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,

REFERENCE
AUTHORS   Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
          Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,
          Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,
          Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,
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          Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,
          Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,
          Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
          Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
          Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
          Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
TITLE   Complete sequencing and characterization of 21,243 full-length
          human cDNAs
JOURNAL   Nat. Genet. 36 (1), 40-45 (2004)
PUBMED   14702039
REFERENCE 2 (bases 1 to 2560)
AUTHORS   Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
          Shibata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
          Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
          Onogawa,S., Keeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
          Kataoka,R., Kuga,N., Kuroda,S., Satoh,I., Kamata,K., Takami,S.,
          Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,
          Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
          Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
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          Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
          Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
          Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 2560)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
          Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
          (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
          Economy, Trade and Industry of Japan; cDNA full insert sequencing:
          Research Association for Biotechnology (RAB); cDNA library
          construction: Helix Research Institute (HRI) (supported by Japan
          Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
          HRI, and Biotechnology Center, National Institute of Technology and
          Evaluation; clone selection for full insert sequencing: HRI and
          RAB; annotation: HRI and RAB.
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ORIGIN

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Pred. No.:
Score: 3.76e-172
Percent Similarity: 198.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 21.85%
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US-10-792-307-4 (1-906) x AK094789 (1-2560)

Length: 2560
Matches: 198
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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Db   2 AGATTCTTCGTGTCCCTGGCCAACTTCTCATCATCTGCTGTTTCTGTGGAAGTGGGTAC 61

Qy 447 LeuIleTyrPheValValLeuAlaLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrp 466
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 CTCATTTACTTTGTGGTTAAGGGATCCAGCAATTCTCCAAAATGCAGAAGTCAGGTGG 121

Qy 467 TyrGluArgAsnGluValGluIleValMetSerLeuLeuGlyMetPheCysProProLeu 486
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 TATGGAAAGGAATGAGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCCTCTG 181

Qy 487 PheGluThrIleAlaIleLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeu 506
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 182 TTTGAAACCATCGCTGCCCTGGAGAATTACCACCCACGGACTGAACTGAAGTGGCAGCTG 241

Qy 507 GlyArgIlePheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAsp 526
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 242 GGACCGCATCTTGCACTCTTCCTGGGGAACCTCTACACATTTCTTCTTGCCCTGATGGAT 301

Qy 527 AspValHisLeuLysLeuAlaAsnGluGluThrIleLysAsnIleThrHisTrpThrLeu 546
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 302 GATGTCCACCTCAAGCTTGCTAATGAGGAGACAATAAAGAACATCACTCACTGGACTCTG 361

Qy 547 PheAsnTyrTyrAsnSerSerGlyTrpAsnGluSerValProArgProProLeuHisPro 566
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 362 TTTAACTATTACAACTCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCT 421

Qy 567 AlaAspValProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeu 586
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 422 GCAGATGTGCCCCGGGGTTCTTGCTGGGAGACAGCTGTGGGCATTGAATTCATGAGGCTG 481

Qy 587 ThrValSerAspMetLeuValThrTyrIleIleThrLeuLeuGlyAspPheLeuArgAla 606
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Db 482 ACGGTGTCCGACATGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCT 541

Qy 607 CysPheValArgPheMetAsnTyrCysTrpCysTrpAspLeuGluAlaGlyPhe 624
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Db 542 TGCTTTGTGCGGGTTCATGAACTACTGCTGGTGCTGGGACTGGAGGCTGGGATTT 595

RESULT 4

CQ850588

LOCUS   CQ850588   3566 bp   DNA   linear   PAT 23-AUG-2004
DEFINITION   Sequence 1057 from Patent EP1447413.
ACCESSION   CQ850588
VERSION   CQ850588.1 GI:51508800
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS   Isogai,T., Yamamoto,J., Nishikawa,T., Isono,Y., Sugiyama,T.,
            Otsuki,T., Wakamatsu,A., Ishii,S., Nagai,K. and Irie,R.
TITLE   Full-length human cDNA
JOURNAL   Patent: EP 1447413-A 1057 18-AUG-2004;
            Research Association for Biotechnology (JP)
FEATURES   Location/Qualifiers
     source   1..3566
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:

Pred. No.:   2.11e-83
Score: 102.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 11.26%
DB: 6

Length: 3566
Matches: 102
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-792-307-4 (1-906) x CQ850588 (1-3566)

Qy   625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyIleuIlePheAsnGlnGly 644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   163 CCTTCATATGCTGAGTTTGATATTAGTGGAAATGTGCTAGGTGTTTGATCTCAACCAAGGA 222

Qy   645 MetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
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Db   223 ATGATCTGGATGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAATGTCCTGCGCCTG 282

Qy   665 LeuThrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684
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Db   283 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCCATGAAAGGC 342

Qy   685 ValPheLysAlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPhe 704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   343 GTGTTCAAAGCCTCCCGGATCCAACACTTCTACATGGGCCTCTTGCTGCTGGTGCTCTTC 402

Qy   705 LeuSerLeuLeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGly 724
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 CTCAGCCTCCTGCCGGTGGCCTACACCATCATGTCCCTCCACCCTCCTTTGACTGCGGGG 462

Qy   725 ProPhe 726
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Db   463 CCCTTC 468

RESULT 5

AK127751

LOCUS   AK127751   3566 bp   mRNA   linear   PRI 19-FEB-2004
DEFINITION   Homo sapiens cDNA FLJ45851 fis, clone OCBBF2018229.
ACCESSION   AK127751
VERSION   AK127751.1 GI:34534796
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
            Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
            Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
            Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
            Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
TITLE   NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 3566)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT   NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: Reverse Proteomics Research Institute, HRI and
            RAB.
FEATURES   Location/Qualifiers
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                     /tissue_type="brain"
                     /dev_stage="fetal"
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     CDS   223..711
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                     /codon_start=1
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                     /translation="MIWMGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPHERVFKA

ORIGIN

Alignment Scores:
Pred. No.:   2.11e-83
Score: 102.00   Length: 3566
Percent Similarity: 100.00%   Matches: 102
Best Local Similarity: 11.26%   Conservative: 0
Query Match: 8   Mismatches: 0
                                                 Indels: 0
                                                 Gaps: 0

US-10-792-307-4 (1-906) x AK127751 (1-3566)

Qy 625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGly 644
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 163 CCTTCATATCCTGAGTTTGATATTAGTGGAAAATGTGCTGGGTTGATCTTCAACCAAGGA 222

Qy 645 MetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 223 ATGATCTGGATGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAATGTCCTGCGCCTG 282

Qy 665 LeuThrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684
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Db 283 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCCATGAACGC 342

Qy 685 ValPheLysAlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuValLeuPhe 704
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Db 343 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCCTCCTGCTCGTGGTCCTCTTC 402

Qy 705 LeuSerLeuLeuProValAlaThrTyrThrIleMetSerLeuProProSerPheAspCysGly 724
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403 CTCAGCCTCCTGCCCGTGGCCACCTACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGG 462

Qy 725 ProPhe 726
         ||||||
Db 463 CCGTTC 468

PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

SRSNNFYMGLLLIVLFLSLLPVAYTIMSLPPSFDCGPFFRCRVSVAREHLPSRGSLLRG
PRPRIPVLVSCQPVKGHGHGTLGESSPMPFKRVFCQDGNVRSFCVCAVHFSSHOPPVAVEC
LK"

ORIGIN

Alignment Scores:
Pred. No.:   4.1e-81
Score: 99.00   Length: 884
Percent Similarity: 100.00%   Matches: 99
Best Local Similarity: 10.93%   Conservative: 0
Query Match: 6   Mismatches: 0
                                                 Indels: 0
                                                 Gaps: 0

US-10-792-307-4 (1-906) x CQ728483 (1-884)

Qy 311 GluGlyTyrIleLysTyrSerSerAlaLeuPheTyrGlyTyrTyrTyrAsnAsnGlnAsnArgThrIle 330
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 187 GAGGGCTATATCAAGTACTCTTCCGCACTCTTCTATGGCTACTACTACAACAACCAGAACCGGACCATC 246

Qy 331 GlyTrpLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGly 350
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 247 GGGTGGCTGAGGTACCGGCTGCCTATGGCTTACTTTATGGTGGGGGTCAGCGTGTTCGGC 306

Qy 351 TyrSerLeuIleIleValIleAlaArgSerMetAlaSerAsnThrGlnGlySerThrGlyGlu 370
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 307 TACAGCCTGATTATTGTCATTGCAAGGAGCATGGCCAGCAATACCCAAGGAAGCACAGGCGAA 366

Qy 371 GlyGluSerAspAsnPhePheSerPhePheLysMetPheThrSerTrpAspTyrLeuIle 390
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 367 GGGGAGAGTGACAACTTCACATTCACGTGGGACTACCTGATC 426

Qy 391 GlyAsnSerGluThrAlaAspAsnLysTyrTyrAlaSerIleThrThrSerPheLysGlu 409
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Db 427 GGGAATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAA 483

TITLE   Dominant and recessive deafness caused by mutations of a novel
          gene, TMC1, required for cochlear hair-cell function
JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
PUBMED   11850618
REFERENCE 2 (bases 1 to 3216)
AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE   Direct Submission
JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
          Rockville, MD 20850, USA
FEATURES   Location/Qualifiers
     source   1..3216
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
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     gene   1..3216
                     /gene="Tmc2"
     CDS   322..2988
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                     /product="transmembrane channel-like protein 2"
                     /protein_id="AAL86402.1"
                     /db_xref="GI:19923985"
                     /translation="MSPQLKSLDEEGDKSARRPTRQTSRAACPQDGHRAQSRKDPA
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                     KKLRELREAQAFVEKYEGALGSKGKGHILVAYRNMMAKKWVFKRDFDNFKTQCIPWEM
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                     RAEEERAMDFSVLWDFEGYIKYSALFYGYYNNQRTIGWLRYRLPMAYFMVGVSVFGYS
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                     RLTVSDMLVTYLTILVGDFLRACFVRFMNHCWCWDLEAGFPSYAEFDISGNVLGLIFN
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ORIGIN

US-10-792-307-4 (1-906) x AF417581 (1-3216)

Alignment Scores:
Pred. No.:   1.14e-80   Length: 3216
Score: 99.00%   Matches: 140
Percent Similarity: 98.59%   Conservative: 0
Best Local Similarity: 98.59%   Mismatches: 1
Query Match: 10.93%   Indels: 2
DB: 9   Gaps: 0

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Qy  213 MetAlaLysLysTrpValPheLysArgAspPheAspAsnPheLysThrGlnCysIle 232
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Db  904 ATGGCTAAGAAAGGGTCAAGTTAAGAGGGACTTCATAATTTCAAGACTCAATGTATT 963

Qy  233 ProTrpGluMetLysIleLysAspIleGluSerHisPheGlySerSerValAlaSerTyr 252
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Db  964 CCCTGGGAAATGAAGATCAAGGACATTGAAAGTCACTTCGGTTCTTCTGTGGCATCTTAC 1023

Qy  253 PheIlePheLeuArgTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024 TTCATCTTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTTGGCTTAATATTTGGT 1083

Qy  273 LeuValIleIleProGluValLeuMetGlyMetProTyrGlySerIleProArgLysThr 292
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Db 1084 CTAGTCATCATCCCAGAGGTGCTGATGGGCATGCCCTATGGAAGTATACCCAGAAAGACG 1143

Qy  293 ValProArgAlaGluGluGluArg-AlaMetAspPheSerValLeuTrpAspPheGluGl 312
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Db 1144 GTGCCTCGAGCTGAGGAAGAGCG-AGCCATGGACTTCTCTGTCCTTTGGGATTTTGAGGG 1202

Qy  312 yTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTr 332
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Db 1203 CTACATCAAATATTCTGCTCTCTTCTATGGCTACTACAACAACCAGCGGACCATTGGATG 1262

Qy  332 pLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyrSe 352
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Db 1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTTATGGTGGGGGTGTCAGGGTGTTTGGCTACAG 1322

Qy  352 rLeu 353
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Db 1323 CTTG 1326
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RESULT 8
HSDJ68C3/c
LOCUS   HSDJ68C3   159272 bp   DNA   linear   PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP4-686C3 on chromosome 20 Contains
            the IDH3B gene for isocitrate dehydrogenase 3 (NAD+) beta, the
            NOL5A gene for nucleolar protein 5A (56kDa with KKE/D repeat), the
            TMC2 gene for transmembrane cochlear expressed protein 2, a novel
            gene, the RNU56 gene for small nuclear RNA U56, the RNU57 gene for
            small nuclear RNA U57, the 5' end of one variant of the ZNF343 gene
            for zinc finger protein 343 and three CpG islands, complete
            sequence.
ACCESSION   AL049712
VERSION   AL049712.12 GI:5629919
KEYWORDS   HTG; C20orf145; CpG island; FLJ37470; IDH3B; isocitrate
            dehydrogenase 3; NOL5A; NOP56; nucleolar protein 5A; RNU56; RNU57;
            small nuclear RNA; TMC2; ZNF343.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 159272)
AUTHORS   Smith,M.
TITLE   Direct Submission
JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT   On Jul 28, 1999 this sequence version replaced gi:5578962.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information

on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
RP4-686C3 is from the library RPCI-4 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2

    Center: Genome Center

    Center: Wellcome Trust Sanger Institute
    Center code: SC
    Web site: http://www.sanger.ac.uk
    Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

FEATURES   Location/Qualifiers
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                     /db_xref="R2PD:RPCIP704C03686"
                     /db_xref="taxon:9606"
                     /chromosome="20"
                     /clone="RP4-686C3"
                     /clone_lib="RPCI-4"

     misc_feature   1
                     /note="Clone_left_end: RP4-686C3"

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     mRNA   complement(join(6075..6691,7343..7597))
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                     /note="match: ESTs: B02181850"

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                     11773..11919,12156..12250,12364..12424,13112..13554)
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                     /locus_tag="RP4-686C3.2-010"
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                     11773..11919,12156..12250,12364..12424,13112..13554)
                     /gene="IDH3B"
                     /locus_tag="RP4-686C3.2-011"
                     /note="match: ESTs: AA087074 AA108496 AA142480 AA167013
                     AA458104 AA599846 AA993092 AI227462 AI272100 AI373206
                     AI609203 AI683664 AI760872 AI830198 AI952254 AL036756

ALS21523 ALS21524 ALS28785 ALS28786 AU117859 AU143386
AU144573 AV596139 AV601328 AV601554 AV608427 AV609363
AV614843 AW168027 AW188413 AW247288 AW289392 AW336378
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BF960054 BF981406 BF982100 BG035393 BG099896 BG111220
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BG671800 BG671964 BG683118 BG683765 BG699984 BG699894
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BG973896 BI086436 BI094428 BI101223 BI180856 BI195335
BI228856 BI328443 BI329344 BI407294 BI407995 BI411628
BI411908 BI414547 BI517745 BI518301 BI526544 BI546520
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BI820012 BI820053 BI820679 BI867811 BI904154 BI904301
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BM143389 BM389346 BM423529 BM451605 BM453562 BM457783
BM458508 BM559953 BM561496 BM563921 BM737944 BM741764
BM742056 BM745323 BM755483 BM750074 BM767961 BM768008
BM806130 BM899930 BM925296 BM978768 BM999950 BN053823
BQ053873 BQ054140 BQ058960 BQ061613 BQ064657 BQ069660
BQ177927 BQ178242 BQ229720 BQ355946 BQ424729 BQ445297
BQ571148 R15323 T49248
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BC001960 BC009022 BC019037 U49283 U87972"

     mRNA   join(7733..7796,7944..8024,8191..8289,8383..8503,
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                     /locus_tag="RP4-686C3.2-008"
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                     10980..11040,11120..11653)
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                     /note="match: ESTs: AW849744 BG001522 BI770850 BM837721
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        10980..11040,11120..11252,11359..11492,11584..11686,
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gene   join(7761..7796,7944..8024,8191..8289,8383..8503,
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CDS   join(7761..7796,7944..8024,8191..8289,8383..8503,
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Score: 95.00   Matches: 95
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 10.49%   Indels: 0
DB: 8   Gaps: 0

US-10-792-307-4 (1-906) x HSDJ686C3 (1-159272)

Qy   28 GlyAspArgLeuGlyArgSerSerSerLysArgAlaLeuLysAlaGluGlyThrPro 47
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113494 GGTGACAGGCTGGGAAGGAGGATCCTCAACCAACGCGGCTCTCAAAGCCGAGGGGACCCCA
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Qy   48 GlyArgArgGlyAlaGlnArgSerGlnLysGluAlaGlyGlySerProSerProGly 67
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Db   113434 GGCAGCGGCGGCGAGCTCAGCGAAGGAGCGGCGCGCGGGGGGGGAGCCCCAAGCCCCGGG
        113375

Qy   68 SerProArgArgLysGlnThrCysGluGlyGlyArgArgArgHisArgGluGluLeuGluGlyLeuGluGlnGlu 87
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113374 TCTTCCCCGGAGGAAGGCAAAACACGGGCCGGGCGCGACACACAGAGAAGAGCTGGGGGAGCAGGAG
        113315

Qy   88 ArgGlyValLeuGluArgThrCysGluGlyGlyArgArgLysArgArgGlyAspGluArgGlyAlaSerPhe 107
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   113314 CGGGGCGGAGGCAGAGAGAGACCTGCGAGGGCCACGAGAAAACGGCCACGAGAGAGGGGCCTCCTTC
        113255

Qy   108 GlnGluArgThrAlaAlaProLysArgGluGluGlyValIleProArgArg 122
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Db   113254 CAGGAGCGGACAGCAGCCCCCAAAGAGGGGAAAAAGGAGATTCCGAGG 113210

RESULT 9
AC156927/c
LOCUS   AC156927   245113 bp   DNA   linear   HTG 01-JUL-2005
DEFINITION   Bos taurus clone CH240-46L23, *** SEQUENCING IN PROGRESS ***, 29
                unordered pieces.
ACCESSION   AC156927
VERSION   AC156927.2   GI:68265339
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE   Bos taurus (cow)
ORGANISM   Bos taurus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                Pecora; Bovidae; Bovinae; Bos.

REFERENCE   1 (bases 1 to 245113)
AUTHORS   Muzny,D.,Marie.,Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
                Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
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Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Micsavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
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Velas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
TITLE   Direct Submission
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 245113)
AUTHORS   Worley,K.C.
TITLE   Direct Submission
JOURNAL   Submitted (05-FEB-2005) Human Genome Sequencing Center, Department
          of Molecular and Human Genetics, Baylor College of Medicine, One
          Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 245113)
AUTHORS   Cow Genome Sequencing Consortium.
TITLE   Direct Submission
JOURNAL   Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
          of Molecular and Human Genetics, Baylor College of Medicine, One
          Baylor Plaza, Houston, TX 77030, USA
COMMENT   On Jun 28, 2005 this sequence version replaced gi:58652284.
          The sequence in this assembly is a combination of BAC based reads
          and whole genome shotgun sequencing reads assembled using Atlas
          (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
          in the feature table below represents a scaffold in the Atlas
          assembly (a 'contig-scaffold'). Within each contig-scaffold,
          individual sequence contigs are ordered and oriented, and separated
          by sized gaps filled with Ns to the estimated size. The sequence
          may extend beyond the ends of the clone and there may be sequence
          contigs within a contig-scaffold that consist entirely of whole
          genome shotgun sequence reads. Both end sequences and whole genome
          shotgun sequence only contigs will be indicated in the feature
          table.

          ------------- Genome Center

          Center: Baylor College of Medicine
          Center code: BCM
          Web site: http://www.hgsc.bcm.tmc.edu/
          Contact: hgsc-help@bcm.tmc.edu

          ------------- Project Information

          Center project name: FCNL
          Center clone name: CH240-46L23

          ------------- Summary Statistics

          Assembly program: Atlas 3.0:
          Consensus quality: 231266 bases at least Q40
          Consensus quality: 234595 bases at least Q30
          Consensus quality: 237389 bases at least Q20
          Estimated insert size: 234838; sum-of-contigs estimation
          Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

          ----

          NOTE: Estimated insert size may differ from sequence length
            (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
          NOTE: This is a 'working draft' sequence. It currently
            consists of 29 contigs. The true order of the pieces
            is not known and their order in this sequence record is
            arbitrary. Gaps between the contigs are represented as
            runs of N, but the exact sizes of the gaps are unknown.
            This record will be updated with the finished sequence
            as soon as it is available and the accession number will
            be preserved.

          *   1   16141: contig of 1641 bp in length
          *   16142   16247: gap of 106 bp
          *   16248   19049: contig of 2802 bp in length
          *   19050   19099: gap of 50 bp
          *   19100   37983: contig of 18884 bp in length
          *   37984   38499: gap of 516 bp
          *   38500   43617: contig of 5118 bp in length
          *   43618   43667: gap of 50 bp
          *   43668   47955: contig of 4288 bp in length
          *   47956   48055: gap of unknown length
          *   48056   52532: contig of 4477 bp in length
          *   52533   53533: gap of 1001 bp
          *   53534   55191: contig of 1658 bp in length
          *   55192   55291: gap of unknown length
          *   55292   75529: contig of 20238 bp in length
          *   75530   76331: gap of 802 bp
          *   76332   100155: contig of 23824 bp in length
          *   100156   100689: gap of 534 bp
          *   100690   120297: contig of 19608 bp in length
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FEATURES   Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9913"
                     /clone="CH240-46L23"
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     • 132376   132425: gap of 50 bp
     • 132426   136897: contig of 4472 bp in length
     • 136898   136947: gap of 50 bp
     • 136948   138345: contig of 1398 bp in length
     • 138346   138395: gap of 50 bp
     • 138396   153574: contig of 15179 bp in length
     • 153575   153624: gap of 50 bp
     • 153625   170313: contig of 16689 bp in length
     • 170314   170363: gap of 50 bp
     • 170364   172270: contig of 1907 bp in length
     • 172271   172320: gap of 50 bp
     • 172321   183412: contig of 11093 bp in length
     • 183413   183463: gap of 50 bp
     • 183464   185804: contig of 2341 bp in length
     • 185805   185854: gap of 50 bp
     • 185855   189962: contig of 4108 bp in length
     • 189963   190012: gap of 50 bp
     • 190013   192069: contig of 2057 bp in length
     • 192070   192119: gap of 50 bp
     • 192120   207009: contig of 14890 bp in length
     • 207010   207109: gap of unknown length
     • 207110   208199: contig of 1090 bp in length
     • 208200   208299: gap of unknown length
     • 208300   209314: contig of 1015 bp in length
     • 209315   209414: gap of unknown length
     • 209415   210544: contig of 1130 bp in length
     • 210545   210644: gap of unknown length
     • 210645   211955: contig of 1311 bp in length
     • 211956   212055: gap of unknown length
     • 212056   213144: contig of 1089 bp in length
     • 213145   213244: gap of unknown length
     • 213245   214652: contig of 1408 bp in length
     • 214653   214752: gap of unknown length
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     • 217958   218057: gap of unknown length
     • 218058   245113: contig of 27056 bp in length.

Alignment Scores:
Pred. No.:   1   Length: 245113
Score: 1.04e-60   Matches: 79
Percent Similarity: 79.00   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 8.72%   Gaps: 0
                           14

US-10-792-307-4 (1-906) x AC156927 (1-245113)

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Db 178527 ATGGGTTCCTTCTACGGCCCCGGGACTGGTGGGCATTAATGTGCTCCGCCTGCTGACCTCC 178468

Qy   668 MetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArgValPheLys 687
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Db 178467 ATGTACTTCCAGTGCTGGGCAGTGATGAGCAGCAACGTCCCCCACGAACGCGTGTTCAAG 178408

Qy   688 AlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuProPheLeuSerLeu 707
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Db 178407 GCCTCCCGCTCCAACAACTTCTACATGGGCCTGCTGCTCCTGGTGCTCCCTTCCTCAGCCTC 178348

Qy   708 LeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGlyProPhe 726
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Search completed: December 5, 2005, 02:29:59
Job time : 10235 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 20:52:17 ; Search time 1129 Seconds
                                        (without alignments)
                                        5348.283 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 906
Sequence: 1 MSHQVKGLKEEARGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Scoring table: OLIGO
                Xgapop 60.0 , Xgapext 60.0
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                Fgapop   6.0 , Fgapext   7.0
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Searched: 4996997 seqs, 3332346308 residues

Word size: 70

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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.1095
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=70 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10792307 @CGN 1.1 1096 @runat_23112005_080814_19754 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_21:*
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             14:    geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
		%				
1	879	97.0	3121	8	ACC69614	Acc69614 Human tra
2	583	64.3	5027	5	AAS92296	Aas92296 DNA encod
3	198	21.9	2560	11	ADM01657	Adm01657 Human cDN
4	153	16.9	2591	6	ABV75613	Abv75613 Human rib
5	102	11.3	3566	13	ADR07551	Adr07551 Full leng
6	99	10.9	3216	8	ACC69616	Acc69616 Mouse tra

ALIGNMENTS

RESULT 1
ACC69614
ID   ACC69614 standard; cDNA; 3121 BP.
XX
AC   ACC69614;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Human transductin-2 (TDC2) encoding cDNA SEQ ID NO:3.
XX
KW   Human; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   16..2688
FT   /*tag= a
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XX
PN   WO2003025140-A2.
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PD   27-MAR-2003.
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PF   19-SEP-2002; 2002WO-US029614.
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PR   19-SEP-2001; 2001US-0323275P.
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PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Griffith AJ, Kurima K, Wilcox E, Friedman T;
XX
DR   WPI; 2003-371806/35.
DR   P-PSDB; ABR43616.

CC The present sequence encodes human transduction-1 and mouse TDC1 and TDC2. The present
CC invention describes human and mouse TDC1 and TDC2. Also described: (1) a
CC method for detecting hearing loss or predisposition to hearing loss in an
CC animal; (2) a method for determining the level of nucleic acid comprising
CC wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
CC sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
CC gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
CC method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
CC TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
CC type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
CC comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
CC and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
CC for treating an animal prophylactically or therapeutically for hearing
CC loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
CC a method for identifying one or more agents that interact with a TDC1
CC and/or TDC2 genes in a cell by administering one or more agents to the
CC cell comprising the genes and assaying the expression level of the genes
CC by the cell, where an increase or decrease in the expression level is
CC indicative of the interaction between the agents and the genes in the
CC cell. TDC1 and TDC2 have auditory activities and can be used in gene
CC therapy. The molecules, compositions and methods of the present invention
CC can be used for prognosticating, treating and monitoring hearing loss
XX
SQ Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 0   Length: 3121
Score: 879.00   Matches: 879
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 97.02%   Indels: 0
DB: 8   Gaps: 0

US-10-792-307-4 (1-906) x ACC69614 (1-3121)

Qy   28 GlyAspProArgLeuGlyArgArgSerSerLysArgAlaLeuLysAlaGluGlyThrPro 47
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   49 GGTGACAGGCTGGGACGGAGAGATCCTCAAGCAACGGGGCCTCTCAAAGCCGAGGGACCCCA 108

Qy   48 GlyArgArgGlyAlaGlnArgSerGlnLysGluArgAlaGlyLySerProSerProGly 67
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   109 GGCAGCGGCGGCGAGCTCAGCGAAGCCAGAAGACGGGAGGCCAGCCCAAGCCCCGGG 168

Qy   68 SerProArgArgLysGlnThrGlyArgArgArgHisArgGluValGluLeuGlyLeuGlu 87
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   169 TCTCCCCGGAGGAAGCAAACAGGGCGGCGGAGACAACAGAGAAAGCTGGGGGACAGAGG 228

Qy   88 ArgGlyGluAlaGluGlyThrCysGluGlyArgArgLysAspGlyTrpArgAlaSerPhe 107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229 CGGGGCGGAGGCAGAAGAGGACCTCGGAGGGAGGAGAAAGGGCCGACGAGGAGGGGCCTCCTTC 288

Qy   108 GlnGluArgThrAlaAlaProLysArgGluArgGlyGluIleProArgLysGlyGluGlySer 127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   289 CAGGAACGGGACAGCAGCCCCAAAGAGGGAAAAGGAGAATTCCGAGGAAGGGGAGTCG 348

Qy   128 LysArgArgGlnLysGlySerProArgSerSerLeuAlaSerSerAlaSerGlyGlyGluSer 147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 AAGCGGCGACAGAAAAACCAGGTCATCCTCCTTGGCGTCCTCCAGTGCGTCCTTCTGGGGGAGTCC 408

Qy   148 LeuSerGluGluLeuAlaGlnIleLeuGluGlnValGluGlyLysLysLysLeuIle 167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   409 CTGTCCGAGGAGGAACTGGCCCAGATCCTGGAGCAGGTGGAAGAAAAAAAGAAGCTCATT 468

Qy   168 AlaThrMetArgSerLysProTrpProMetAlaLysLysLeuThrGluLeuArgGluAla 187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469 GCCACCATGCGGAGCAAGCCCTGGCCCATGGCCAAGAAGCTGACAGAGCTCAGGGAGGCC 528

Qy   188 GlnGluPheValGlyLysTyrGluGlyValAlaLeuGlyLysGlyLysGlyGlnGlnLeuTyr 207
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 CAGGAATTTGTGGGAAAGTATGAAGGTGCCTGGGAAAGGGGAAAGGGCAAGGCAAACTATAT 588

Qy   208 AlaTyrLysMetLeuMetAlaLysLysTrpGluValArgArgPheAspAsnPhe 227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   589 GCCTACAAGATGCTGATGGCCAAGAAATGGGTCAAATTAAGGAGGACTTTGATAATTTC 648

Qy   228 LysThrGlnCysIleProGluMetLysIleLysSerHisPheGlySer 247
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db   649 AAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGGACCATTGAAAGTCACTTTGGTTCT 708

Qy   248 SerValAlaSerTyrPhePheLeuArgTrpMetTyrGlyValAsnLeuValLeuPhe 267
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   709 TCAGTGGCATCCTATTTCATCTTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTT 768

Qy   268 GlyLeuIlePheGlyLeuValIleIleProGluValLeuMetGlyMetProTyrGlySer 287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   769 GGCTTAATATTTGGTCTAGTCATAATCCCAGAGTTACTCATGGGTACTACAACAACCAG 828

Qy   288 IleProArgGlyThrValProArgAlaGluLeuGluGlyLysAlaMetAspPheSerValLeu 307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   829 ATTCCCAGAAAGACAGTGCCTCGGGCTGAGGAGAAAGGGCCATGGATTTTCTGTCCTT 888

Qy   308 TrpAspPheGluLeuGlyTyrIleLeuLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGln 327
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   889 TGGGATTTTGAGGGGTATATCAAGTACTCTGCACTCTTCTATGGCTACTACAACAACCAG 948

Qy   328 ArgThrIleGlyTrpLeuArgTyrArgLeuProMetGlyTyrPheMetValGlyValSer 347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   949 AGGACCATCGGGTGGCTGAGGTACCGGCTGCCTATGGGCTACTTTATGGTGGGGGTCAGC 1008

Qy   348 ValPheGlyTyrSerLeuIleIleValIleIleArgSerMetAlaSerAsnThrGlnGlySer 367
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1009 GTGTTCGGCTACAGCCTGATTATTGTCATTCGCAGCATGGCCAGCAATACCCAGGGAAGC 1068

Qy   368 ThrGlyGluGlyGluSerAspAsnPheThrPheSerPheLysMetPheThrSerTrpAsp 387
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1069 ACAGGCGAAGGGGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGAC 1128

Qy   388 TyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyrAlaSerIleThrThrSerPhe 407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TACCTGATCGGGAATTCAGAGACTGATAACAAATATGGATCCATCACCACCAGCTTC 1188

Qy   408 LysGluSerIleValAspGluGlnSerAsnLysGluAsnIleHisLeuThrArg 427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 AAGGAATCAATAGTGGATGAACAGAGTAACAAAGAGAATATCCATCTGACAAGA 1248

Qy   428 PheLeuValLeuAlaAsnPheLeuIleIleCysCysLeuCysGlySerGlyTyrLeu 447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 TTTCTTCGTGTCTGGGCCAACTTTCTCATCATCTGTTGTGTCTGGAAGTGGGTACCTC 1308

Qy   448 GluArgAsnGluValGluIleValMetSerLeuLeuGlyMetPheCysProLeuPhe 467
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 ATTTACTTTGTGGTTAAGCGAATCTCAGCAATTCTCCAAAATGCAGAATGTCAGCTGGTAT 1368

Qy   468 GluValAspGluGlnSerGlnAsnPheSerLeuArgMetGlnAsnValSerTrpTyr 487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 GAAAGGAATGAGGTAGAGAATCGTAGTCCCTGCTTGGAATGTTTGTCCCCCTCTGTT 1428

Qy   488 GluThrIleAlaAlaLeuGluAsnTyrHisProArgThrGlyLeuGlyLysTrpGlnLeuGly 507
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GAAACCATCGCTGCCCTGGGAGAATTACCACCCACGACTGGACTGGGCAGGTAATGCC 1488

Qy   508 ArgIlePheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAsp 527
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Db   1489 CGGATCTTTGCACTCTTCCTGGGCAACCTCTACACATTTCTTCTGGCCCTGATGGATGAC 1548

Qy   528 ValHisIleLeuLysAlaAsnGluGluThrIleLysLysTyrAsnIleThrHisTrpThrLeuPhe 547
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 GTCCACCTCAAGGCTTGCTAATGAAGAACAATAAAGAACATCACTCACTGGACTCTGTT 1608

Qy   548 AsnThrTyrArgAsnSerSerGlyTyrTrpAsnGluSerValProArgProProLeuHisProAla 567
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 AACTATTACAACTCTCTGGTTGGAACGAGGTGTCCCCGACCACCCCTGCCACCTGCA 1668

Qy   568 AspValProArgGlySerCysTrpGluThrAlaValGlyValIleGluLeuThr 587
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Db   1669 GATGTGCCCCGGGGTTCTTGCTGGGACAGAGCTGTGGGCATTGAATTCATAGGCTGACG 1728

Qy   588 ValSerAspMetLeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAlaCys 607
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Db   1729 GTGTCTGACATGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCTTGT 1788

Qy   608 PheValArgPheMetAsnTyrCysTrpCysTrpAspLeuGluAlaGlyTyrPheProSerTyr 627
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Db   1789 TTTGTGCGGTTCATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGGATTTTTCCTTCATAT 1848

Qy   628 AlaGluProAspSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrp 647
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Db   1849 GCTGAGTTTGATATTAGTGGAAATGTCCTGGGTTTGATCTTCAACCAAGGAATGATCTGG 1908

Qy   648 MetGlySerPheTyrAlaProGlyLeuValGlyTyrIleAsnValLeuArgLeuLeuThrSer 667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 ATGGGGTCCTTCTATGCTCCAGGCCTGGTGGGGTATATAAATGTGCTGCGCCTTCTGACCTCC 1968

Qy   668 MetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArgValPheLys 687
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 ATGGGCTCCAGTGCTGCTGGGCGGTGATGAGCAGCAACGTACCCCATGAAGGCGTTGTTCAAA 2028

Db   1969 ATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCCATGAAGGCGTTGTTCAAA 2028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   688 AlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuLeuValLeuPheLeuSerLeu 707
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 GCCTCCCGGATCCAACAACTTCTACATGGGCCTCCTGCTCCTGCTGGTGCTTCTGCAGCTC 2088

Qy   708 LeuProValAlaTyrThrIleMetSerLeuProSerPheAspCysGlyGlyProPheSer 727
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Db   2089 CTGCCCGGTGGCCTACACCATCATGTCCCTCCCAAGCTTCGTGGCGGGCCGTTCAGT 2148

Qy   728 GlyLysAsnArgMetTyrAspAspValLeuGlnGluThrIleGluAsnAspPheProThrPhe 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 GGGAAAAACAGAATGTACGATGTCCTCCAAGAGACCATTGAAAACGATTTCCCAACCTTC 2208

Qy   748 LeuGlyIleGlyLeuLeuLeuAlaAsnProGlyLeuIleLeuIleLeuAlaIleLeuLeu 767
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 CTGGGCATCGGATCTTTGCTTCTGGCCAATCCAGGGCTGATCCTGATCCTAGCTATCCTGCTG 2268

Qy   768 MetPheLeuLeuAlaIleTyrTyrLeuAsnSerValSerLysSerLeuSerArgAlaAsnAla 787
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 ATGTTCTTGCCATTTACCTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCC 2328

Qy   788 GlnLeuArgGlyLysIleGlnValLeuLeuArgGluValGlyLysSerHisLysLysSerValLys 807
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 CAGCTGAGGAACAAAATCCAAGTGCTCCGTGAAGTTGAGAAGAGTCACAAAATCTGTAAAA 2388

Qy   808 GlyLysAlaThrAlaAlaArgAspSerGluAspThrProLysSerSerSerLysLysAsnAlaThr 827
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 GGCAAAGCCACAGCCGAGATTCAGAGGACACACCACCTAAAAGGGACTCCAAAAATGCCACC 2448

Qy   828 GlnLeuGlnLeuThrLeuLysGluLeuThrThrProProSerProAlaSerGlnSerGlnAlaMet 847
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 CAGCTCCAACTCACCAAGGAAGAGACCACTCCTCCTCCTCCAGCCCAAAGCCAGGCCATG 2508

Qy   848 AspLysLysAlaGlnGlyProGlyTyrThrSerAsnSerAlaSerArgThrThrLeuProAla 867
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 GACAAGAAAGCCCAGGGCCCTGGGACCTCCAATTCTGCCAGCAGACCACACTGCTGCC 2568

Qy   868 SerGlyHisLeuProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaPro 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 TCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGACCAGATTCTGGCCACGCCCCA 2628

Qy   888 SerGlnThrHisSerProThrProArgSerAlaSerGlyValSerAlaGlnAlaArgProHis 906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 TCTCAGACTCATCCCGTGGAAGTCAGCCTCTGGAAAGAGAGTGCTCAGAGACCTCCCAC 2685

Alignment Scores:

Pred. No.:   0
Score: 583.00   Length: 5027
Percent Similarity: 100.00%   Matches: 583
Best Local Similarity: 100.00%   Conservative: 0
                                            Mismatches: 0

Query Match: 64.35%   Indels: 0
DB: 5   Gaps: 0

US-10-792-307-4 (1-906) x AAS92296 (1-5027)

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Qy  312 GlyTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGly 331
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1096 GGCTATATCAAGTACTACTGCACTCTTCTTCTATGGCTACTACAACAACGAGGACCATCGGG 1155

Qy  332 TrpLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyr 351
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1156 TGGCTGAGGTACCGGCTGCCTATGGCCTACTTTATGGTGGGGGTCAGCGTGTTCGGGTAC 1215

Qy  352 SerLeuIleIleValIleLeuArgSerMetAlaSerAsnThrGlnGlnGlySerThrGlyGluGly 371
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1216 AGCCTGATTATTGTCATTCGATCGATGGCCAGCAATACCCAGCAGGGAAGCACAGGCGAAGGG 1275

Qy  372 GluSerAspAsnPheThrPheSerPheLysMetPheThrSerTrpAspTyrLeuIleGly 391
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Db 1276 GAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGACTACCTGATCGGG 1335

Qy  392 AsnSerGluThrAlaAlaAspAsnLysTyrAlaSerIleThrThrSerProPheLysGluSerIle 411
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Db 1336 AATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATA 1395

Qy  412 ValAspProGlnGlyGluSerAsnLysGluGluGlnAsnIleHisLeuThrArgPheLeuArgVal 431
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Db 1396 GTGGATGAACAAGGAGAGTAACAAAGAGGAAAATATCCATCTGACAAGATTTCTTCGTGTC 1455

Qy  432 LeuAlaAsnPheLeuIleIleCysCysLeuCysGlySerGlyTyrLeuIleTyrPheVal 451
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1456 CTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTGTG 1515

Qy  452 ValLysArgSerGlnPheSerGlyMetGlnAsnValSerTrpTyrGluArgAsnGlu 471
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Db 1516 GTTAAGGCGATCTCAGCAATTCTCCAAAATGCAGAATGTCAGCTGGTATGAAAGGAATGAG 1575

Qy  472 ValGlyIleLeuValMetSerLeuLeuGlyMetPheCysProProLeuPheGluThrIleAla 491
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Db 1576 GTAGGAATCCTGGTCATGTCCCTGCTTGGAATGTTTTGTCCCCCTCGTTTGAAAACCATCGCT 1635

Qy  492 AlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGlyArgIlePheAla 511
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Db 1636 GCCCTGGAGAATTACCACCCACGGACTGGACTGAAGTGGCAGCTGGGACGCATCTTTGCA 1695

Qy  512 LeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAspValHisLeuLys 531
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Db 1696 CTCTTCCTGGGGAACCTCTACACATTTCTTCTGGCCCTGATGGATGACGTCCACCTCAAG 1755

Qy  532 LeuAlaAsnGluGlnThrIleLysAsnIleThrHisTrpThrLeuPheAsnTyrTyrAsn 551
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Db 1756 CTTGCTAATGAAGAGACAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACAAC 1815

Qy  552 SerSerGlyTrpProAsnGluSerValProArgProProLeuHisProAlaAspValProArg 571
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Db 1816 TCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCAGATGTGCCCCCG 1875
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Qy   572 GlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeuThrValSerAspMet 591

Db   1876 GGTTCTTGCTGGGAGACAGCTGTGGGAGCATTGAATTCATGAGGCTGACGGTGTCTGACATG 1935

Qy   592 LeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAlaCysPheValArgPhe 611

Db   1936 CTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCTTGTTTTGTCCGGTTC 1995

Qy   612 MetAsnTyrCysTrpCysTrpAspLeuGluValGlyPheProSerTyrAlaGluPheAsp 631

Db   1996 ATGAACTACTGCTGGTGCTGGGACTTGGAGGTCGGATTTCCTTCATATGCTGAGTTTGAT 2055

Qy   632 IleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrpMetGlySerPhe 651

Db   2056 ATTAGTGGAAATGTCCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCTTC 2115

Qy   652 TyrAlaProGlyLeuValGlyIleAsnValLeuArgLeuLeuThrSerMetTyrPheGln 671

Db   2116 TATGCTCCAGGCCTGGTGGGCATTAATGTGCTGCGGCTGCTGACCTCCATGTACTTCCAG 2175

Qy   672 CysTrpAlaValMetSerSerAsnValProHisGluArgValPheLysAlaSerArgSer 691

Db   2176 TGCTGGGCGGTGATGAGCAGCAACGTACCCCATGAACGGGTGTTCAAAGCCTCCCGGATCC 2235

Qy   712 TyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSerGlyLysAsnArg 731

Db   2236 AACGACTTCTACATGAGCGGCTTCTCCTGTCGTGCTTCTTCCTCAGCCTTCCTGGGTGGCC 2295

Qy   692 AsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPheLeuSerSerLeuProValAla 711

Db   2296 TACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGCCGTTCAGTGGGAAAAAACAGA 2355

Qy   732 MetTyrAspValLeuGlnGluThrIleGluAsnAspPheProThrPheLeuGlyIle 751

Db   2356 ATGTACGATGTCCTCCAAGAGACCATTGAAAACGATTTCCCAACCTTCCTGGGCAAGATC 2415

Qy   752 PheAlaPheLeuAlaAsnProGlyLeuIleIlePheProAlaIleLeuLeuMetPheLeuAla 771

Db   2416 TTTGCTTTCCTCGCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTTATGTTCTTGGCC 2475

Qy   772 IleTyrTyrLeuAsnSerValSerLysSerLeuSerArgAlaAsnAlaGlnLeuArgLys 791

Db   2476 ATTTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCCCAGCTGAGGAAG 2535

Qy   792 LysIleGlnValLeuArgGluValGluHisLysSerSerValLysGlyLysAlaThr 811

Db   2536 AAAATCCAAGTGCTCCGTGAAGTTGAGCACAAATCTGTAAAAGGCAAAGCCACA 2595

Qy   812 AlaArgAspSerGluSerProGlySerSerSerLysLysAsnAlaThrGlnLeuGlnLeu 831

Db   2596 GCCAGAGATTCAGGAGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCTCCAACTC 2655

Qy   832 ThrLysGluGluThrThrProProSerAlaSerGlnSerGlnAlaMetAspGlyLysAla 851

Db   2656 ACCAAGGAAGAGAACAACACCTCCTCCTTGCCAGCCCAAAGCCATGGACACAGAGAGGCG 2715

Qy   852 GlnGlyProGlyTyrThrSerAsnSerAlaSerArgThrThrLeuProAlaSerGlyHisLeu 871

Db   2716 CAGGGGCCCTGGGACCTCCAAATTCTGCCAGCAGAGACCACACTGCCTGCCTTCTGGACACTT 2775

Qy   872 ProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaProSerArgGlnThrHis 891

Db   2776 CCTATATCTCGGCCCCCCTGGAATCGGACCCAGAGTTCTGGCCACGCCCACCCCATCTCAGACTCAT 2835

Qy   892 ProTrpProArg 894

Db   2836 CCCTGGAGA 2844

RESULT 3

ADM01657
ID   ADM01657 standard; cDNA; 2560 BP.
XX
AC   ADM01657;
XX
DT   20-MAY-2004 (first entry)
XX
DE   Human cDNA of the invention SEQ ID NO:342.
XX
KW   ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
OS   Homo sapiens.
XX
PN   EP1347046-A1.
XX
PD   24-SEP-2003.
XX
PF   12-APR-2002; 2002EP-00008400.
XX
PR   22-MAR-2002; 2002JP-00137785.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI   Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI   Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR   WPI; 2003-723558/69.
DR   P-PSDB; ADM04100.
XX
PT   New polynucleotides and polypeptides are useful in gene therapy, for
PT   developing a diagnostic marker or medicines for regulating their
PT   expression and activity, or as a target of gene therapy.
XX
PS   Claim 1; SEQ ID NO 342; 305pp; English.
XX
CC   The invention relates to a novel human polynucleotide and the encoded
CC   polypeptide. A polynucleotide of the invention may have a use in gene
CC   therapy. An oligonucleotide of the invention ADM062202-ADM06773 is useful
CC   as a primer for synthesizing the polynucleotide or as a probe for
CC   detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC   useful in gene therapy, for developing a diagnostic marker or medicines
CC   for regulating their expression and activity, or as a target of gene
CC   therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC   are useful as pharmaceutical agents. The present sequence represents a

```
CC   cDNA sequence of the invention.
XX
SQ   Sequence 2560 BP; 568 A; 652 C; 568 G; 772 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                    2.96e-179      Length:              2560
Percent Similarity:       198.00         Matches:             198
Best Local Similarity:    100.00%        Conservative:        0
Query Match:              100.00%        Mismatches:          0
DB:                       21.85%         Indels:              0
                          11             Gaps:                0

US-10-792-307-4 (1-906) x ADM01657 (1-2560)

Qy  427 ArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysCysLeuCysGlySerGlyTyr 446
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 AGATTTCTTCGTGTCCTGGCCAACTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTAC 61

Qy  447 LeuIleTyrPheValValLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrp 466
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 CTCATTTACTTTGTTGGTTAAGCCAATCTCAGCAATTCTCCAAAATGCAGAAAGTCAGCTGG 121

Qy  467 TyrGluArgAsnGluValGlyIleValMetSerLeuLeuLeuGlyMetPheCysProProLeu 486
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122 TATGAAAAGAATGAGGTAGAGAATCGTGATCTCCCTGCTTGGAANGTTTTGTCCCCCTCTG 181

Qy  487 PheGluThrIleAlaAlaAlaLeuGluAsnTyrHisProArgThrGlyLeuLeuTyrGlnLeu 506
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  182 TTTGAAACCATCGGTCGCCTGGAGAATTACCACCCACGCACTGGACTGAAGTGGCAGCTG 241

Qy  507 GlyArgIlePheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuWalAlaLeuMetAsp 526
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  242 GGACCGCATCTTTGCACTCTTCCTCGGGGAACCCTACACATTTCTTCTTGGGCCTGATGGAT 301

Qy  527 AspValHisLeuLysLeuAlaAsnGluGluThrHisThrThrLeu 546
            |||||||||||||||||||||||||||||||||||||||||||||
Db  302 GATGTCCACCTCAAGCTTGCTAATGAAGAGACAATAAAGAACATCACTCACTGGACTCTG 361

Qy  547 PheAsnTyrTyrAsnSerSerGlyTrpAsnGluSerValProArgProProLeuHisPro 566
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  362 TTTAACTATTACAACTCTCTCGGTTGGACGAGAGTGTCCCCGACACCCCTGCACCCT 421

Qy  567 AlaAspValProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeu 586
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  422 GCAGATGTGCCCCGGGGTTCTTGCTGGGAGACAGCTGTGGGCATTGAATTCATGAGGCTG 481

Qy  587 ThrValSerArgMetLeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAla 606
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  482 ACGGTGTCCGACATGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCT 541

Qy  607 CysPheValArgPheMetAsnTyrCysTrpCysTrpAspLeuGluAlaLeuGlyPhe 624
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  542 TGTTTTGTGCGGTTCATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGGATTT 595
```

```
RESULT 4
ABV75613
ID   ABV75613 standard; cDNA; 2591 BP.
XX
AC   ABV75613;
XX
DT   23-JAN-2003  (first entry)
XX
DE   Human ribosomal protein L3220.9 cDNA.
XX
KW   Human; ribosomal protein L3220.9; diabetes; menstrual disorder; anaemia;
KW   peptic ulcer; arrhythmia; epilepsy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..646
FT                   /tag= a
FT                   /product= "Ribosomal protein L3220.9"
XX
PN   CN1345827-A.
XX
PD   24-APR-2002.
XX
PF   29-SEP-2000; 2000CN-00125511.
XX
PR   29-SEP-2000; 2000CN-00125511.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y, Xie Y;
XX
PT   Novel polypeptide-human ribosomal protein L3220.9 and encoding
PT   polynucleotide for treating diabetes, menstrual disorder, peptic ulcer,
PT   arrhythmia, anemia and epilepsy.
XX
PS   Claim 6; Page 25-26 (Disclosure); 33pp; Chinese.
XX
CC   The invention relates to the novel human ribosomal protein L3220.9, and
CC   the polynucleotide encoding it. The protein is useful for treating
CC   diabetes, menstrual disorder, peptic ulcer, arrhythmia, anaemia and
CC   epilepsy. Also disclosed is an antagonist for resisting the polypeptide
CC   and its therapeutic action, and the application of the polynucleotide.
CC   The present sequence encodes the human ribosomal protein L3220.9 of the
CC   invention
XX
SQ   Sequence 2591 BP; 576 A; 670 C; 557 G; 788 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score:                    4.67e-136      Length:              2591
Percent Similarity:       153.00         Matches:             153
Best Local Similarity:    100.00%        Conservative:        0
Query Match:              100.00%        Mismatches:          0
DB:                       16.89%         Indels:              0
                          6              Gaps:                0

US-10-792-307-4 (1-906) x ABV75613 (1-2591)
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Qy 472 ValGluIleValMetSerLeuLeuGlyMetPheCysProProLeuPheGluThrIleAla 491
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 GTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCTCTGTTTGAAACCATCGCT 121

Qy 492 AlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGlyArgIlePheAla 511
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GCCCTGGAGAATTACCACCCAGGCACTGGACTGAAGTGGCAGCTGGGACGCATCTTTGCA 181

Qy 512 LeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAspValHisLeuLys 531
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 182 CTCTTCCTGGGGAACCTCTACACATTTCTCTTGGCCCTGATGGATGATGTCCACCTCAAG 241

Qy 532 LeuAlaAsnGluGluThrIleLysAsnIleThrHisTrpThrLeuPheAsnTyrTyrAsn 551
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 242 CTTGCTAATGAAGGAGACAATAAAGAACATCACTCACTCGGACTCTGTTTAACTAATACAAC 301

Qy 552 SerSerGlyTrpAsnGluSerValProArgProProLeuHisProAlaAspValProArg 571
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 302 TCTTCTGGTTGGAACGAGAGTGTCCCCAGACCACCCCTGCACCCTGCAGATGTGCCCCGG 361

Qy 572 GlySerCysTrpGluThrAlaValGlyIleGluProHisMetArgLeuThrValSerAspMet 591
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 362 GGTTCTTGCTGGGAGACAGCGGTGGGCATTGAATTCATGAGGCTGACGGTGTCCGACATG 421

Qy 592 LeuValThrTyrIleThrThrLeuLeuGlyAspPheLeuArgPheLeuAlaCysPheValArgPhe 611
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 422 CTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCTTCGTTTGTCCGGTTC 481

Qy 612 MetGlnAsnTyrCysTrpAspLeuGluAlaGlyPhe 624
|||||||||||||||||||||||||||
Db 482 ATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGGATT 520

RESULT 5
ADR07551
ID ADR07551 standard; cDNA; 3566 BP.
XX
AC ADR07551;
XX
ADR07551;
XX
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for treating neurological disease Seq 1057.
XX
KW gene; 55; human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquiliser.
XX
OS Homo sapiens.
XX
PN EP1447413-A2.
XX
PD 18-AUG-2004.
XX
PF 12-FEB-2004; 2004EP-0003145.

XX
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
DR WPI; 2004-583265/57.
DR P-PSDB; ADR09507.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 1057; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC cytostatic and tranquiliser activities. This polynucleotide is a full
CC length human cDNA sequence of the invention. NOTE: This sequence is not
CC given in the sequence listing of the specification but can be obtained on
CC CD-ROM from the European Patent Office, Vienna Sub-office.
XX
SQ Sequence 3566 BP; 989 A; 791 C; 877 G; 909 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   5.7e-87   Length: 3566
Score: 102.00   Matches: 102
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 11.26%   Indels: 0
DB: 13   Gaps: 0

US-10-792-307-4 (1-906) x ADR07551 (1-3566)

Qy 625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGly 644
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 163 CCTTCATATGCTGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGGA 222

Qy 645 MetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 223 ATGATCTGGATGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAATGTGCTGCGCCTG 282

Qy 665 LeuThrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 283 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGGAGCAACGTACCCATGAACGC 342
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 685 ValPheLysAlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPhe 704
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 343 GTGTTCAAAGCCTCCGATCCAAGACAACTTCTACATGGGCCTCCTTGCTGCTGGTGCTTC 402
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 705 LeuSerLeuLeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGly 724
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 403 CTCAGGCTCCTGCCGGTGGCGTACACCATCATGTCCCTGCCACCCTCCTTTGACTGCGGG 462
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 725 ProPhe 726
Db ||||||
Db 463 CCGTTC 468

RESULT 6
ACC69616
ID   ACC69616 standard; cDNA; 3216 BP.
XX
AC   ACC69616;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Mouse transductin-2 (TDC2) encoding cDNA SEQ ID NO:7.
XX
KW   Mouse; transductin-2; TDC2; hearing loss; auditory; gene therapy; gene;
      ss.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT
FT   CDS   322..2988
FT   /*tag= 8
FT   /product= "transductin-2"
XX

PN   WO200302540-A2.
XX
PD   27-MAR-2003.
XX
PF   19-SEP-2002; 2002WO-US029614.
XX
PR   19-SEP-2001; 2001US-0322275P.
XX
PA   (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Griffith AJ, Kurima K, Wilcox E, Friedman T;
XX
DR   WPI; 2003-371806/35.
DR   P-PSDB; ABR43618.
XX
PT   An isolated or purified nucleic acid molecule encoding transductin-1
PT   (TDC1), TDC2, or its fragment, useful for prognosticating, treating or
PT   monitoring hearing loss.
XX
PS   Claim 10; Fig 4; 85pp; English.
XX
CC   The present sequence encodes mouse transductin-2 (TDC2). The present
CC   invention describes human and mouse TDC1 and TDC2. Also described: (1) a
CC   method for detecting hearing loss or predisposition to hearing loss in an
CC   animal; (2) a method for determining the level of nucleic acid comprising
CC   wild-type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test
CC   sample comprising a nucleic acid comprising the wild-type TDC1 or TDC2
CC   gene and/or mutant TDC1 or TDC2 gene obtained from the animal; (3) a
CC   method for detecting the level of wild-type TDC1 or TDC2, and/or mutant
CC   TDC1 or TDC2 in a test sample comprising a protein comprising the wild-
CC   type TDC1 or TDC2 gene and/or mutant TDC1 or TDC2 gene in a test sample
CC   comprising a nucleic acid comprising the wild-type TDC1 or TDC2 gene
CC   and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
CC   for treating an animal prophylactically or therapeutically for hearing
CC   loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
CC   a method for identifying one or more agents that interact with a TDC1
CC   and/or TDC2 genes in a cell by administering one or more agents to the
CC   cell comprising the genes and assaying the expression level of the genes
CC   by the cell, where an increase or decrease in the expression level is
CC   indicative of the interaction between the agents and the genes in the
CC   cell. TDC1 and TDC2 have auditory activities and can be used in gene
CC   therapy. The molecules, compositions and methods of the present invention
CC   can be used for prognosticating, treating and monitoring hearing loss
XX
SQ   Sequence 3216 BP; 847 A; 808 C; 813 G; 748 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:
Score: 3.91e-84   Length: 3216
Percent Similarity: 99.00   Matches: 140
Best Local Similarity: 98.59%   Conservative: 0
Query Match: 98.59%   Mismatches: 1
DB: 10.93%   Indels: 2
                                     Gaps: 0

US-10-792-307-4 (1-906) x ACC69616 (1-3216)

Qy 213 MetAlaLysLysTrpValLysPheLysArgAspAsnPheLysThrGlnCysIle 232
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 904 ATGGCTAAGAAATGGGTCAAGTTTAAGAGGGACTTTGATAATTTCAAGACTCAATGTATT 963

Qy 233 ProTrpGluMetGlyIleLysAspIleGluSerHisPheGlySerSerValAlaSerTyr 252
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 964 CCCTGGGAAATGAAGATCAAGGACATTGAAAGTCACTCGGGTTCTTCTGTTGGCATCTTAC 1023

Qy 253 PheIlePheLeuLeuArgTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1024 TTCATCTTTCTCCGATGATGTATGGAGTTAACCTTGTCCTTTTGGCTTAATATTTGGT 1083

Qy 273 LeuValIleIleProGluValValMetGlyMetProTyrGlySerIleProArgLysThr 292
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1084 CTAGTCATCATCCCAGAGGTCGTGATGGGCATGCCCTATGGAAGTATACCCAGAAAGACG 1143

Qy 293 ValProArgAlaGluGluGluLys-AlaMetAspPheSerValLeuTrpAspPheGluGl 312
Db ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 1144 GTGCCTCGAGCTGAGGAAGAGGCG-AGCCATGGACTTCTCTGTCCTTTGGGATTTTGAGGG 1202

Qy 312 yTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrArgAsnAsnGlnArgThrIleGlyTyr 332
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1203 CTACATCAAATATTCTGCTCTCTTCTATGGGTACTACAGAAACAACCAGCGGACCATTGGATG 1262

```
Qy      332 pLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyrSe 352
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1263 GCTGAGGTACAGGCTGCCCATGGCTTACTTTATGGTGGGGGTCAGCCTGTTTGGCTACAG 1322

Qy      352 rLeu 353
            ||||
Db     1323 CTTG 1326
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Job time : 1147 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 23:18:08 ; Search time 380 seconds
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Title: US-10-792-307-4
Perfect score: 906
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                 Fgapop   6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 1303057 seqs, 888780828 residues

Word size: 70

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing; Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result             Query
No.    Score   Match Length DB   ID                    Description
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No matches found

Search completed: December 5, 2005, 04:35:25
Job time : 380 secs

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Perfect score: 906
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                Ygapop   60.0 , Ygapext 60.0
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Searched: 9793542 seqs, 4134689005 residues

Word size: 70

Total number of hits satisfying chosen parameters: 7

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Post-processing: Listing first 45 summaries

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                6: /cgn2_6/ptcdata/1/pubpna/US10B_PUBCOMB.seq:*
                7: /cgn2_6/ptcdata/1/pubpna/US10C_PUBCOMB.seq:*
                8: /cgn2_6/ptcdata/1/pubpna/US10D_PUBCOMB.seq:*
                9: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*
               10: /cgn2_6/ptcdata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	906	100.0	3169	9	US-10-792-307-3	Sequence 3, Appli
2	879	97.0	3121	8	US-10-487-887-3	Sequence 3, Appli
3	583	64.3	4895	6	US-10-115-831-134	Sequence 134, App
4	583	64.3	5027	9	US-10-450-763-28100	Sequence 28100, A
5	198	21.9	2560	6	US-10-108-260A-342	Sequence 342, App
6	99	10.9	3216	8	US-10-487-887-7	Sequence 7, Appli
7	99	10.9	3216	9	US-10-792-307-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-792-307-3

; Sequence 3, Application US/10792307
; Publication No. US20050196759A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J.
; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 227540
; CURRENT APPLICATION NUMBER: US/10/792,307
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 3
; LENGTH: 3169
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-792-307-3 (1-906) x US-10-792-307-3 (1-3169)

Alignment Scores:

Pred. No.:	0	Length:	3169
Score:	906.00	Matches:	906
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
DB:		Gaps:	0

US-10-792-307-4

Qy   1 MetSerHisGlnValLysGlyLeuLysGluGluValaArgGlyGlyValLysGlyArgVal 20
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Db   16 ATGAGCCACCAGTAAAGGGCCTGAAAGAGGAGAAGAGGGCCCAGGCGCGAGTGAAAGGCGGGGGTG 75

Qy   21 LysSerGlySerProHisThrGlyAspArgLeuGlyArgArgSerSerLysArgAla 40
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Db   76 AAGAGCGGGCGTCTCCACACACGTGGACAGGCTGGGAAGGAGAGATCTCAAGCAAGCGGGCT 135

Qy   41 LeuLysLysAlaGluGlyThrProGlyArgArgGlyAlaGlnArgSerGlnLysGluArgAla 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 136 CTCAAAGCCGAGGGGACCCCAGGCAGGCGCGGGAGCTCCAGGCAAGGAGCGCGCGCC 195

Qy   61 GlyGlySerProSerProGlySerProArgArgLysGlnThrGlyArgArgArgHisArg 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 196 GGGGGCAGGCAGCCCAAGCCCGGGGTCCCCCGGAGGAAGCAAACAGGGCGGCGAGGACACAGA 255

Qy   81 GluGluLeuGlyGluGlnGluArgGluValAlaGluArgThrCysGluGlyArgArgGlyLys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 256 GAAGAGCTGGGGAGCAGGAGCGGGAAGGGAGGCAGAGGGGACCTGCGAGGGGAGAAAG 315

Qy 101 ArgAspGluArgGlnAlaSerPheGlnLeuArgThrAlaAlaProLysArgGlyLysGluIle 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 316 CGCGACGAGAGGCAGGCCTCCTTCCAGGAGCGGACAGCAGCCCCAAAGAGGGAAAGGAGATT 375

Qy 121 ProArgLysGluGluGluLysSerArgGlnLysLysLysProArgSerSerLeuAlaSer 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 376 CCGAGGAAGGAGGAGAAGTCGAAGCAGGGCCAGAAGAAAACCAGGTCATCCTTCCTTGGCCTCC 435

Qy 141 SerAlaSerGlyGlyGluSerGluSerGluGluGluLeuAlaGluIleIleLeuGlnValVal 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 436 AGTGCCTCTGGTGGGGAGTCCGTCCGTCCGAGGAGGAACTGGCCGAGATCCTGAGCAGGAGGTG 495

Qy 161 GluGluLysLysLysLysGlyLeuIleAlaThrMetArgSerLysProTrpProMetAlaLys 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 496 GAAGAAAAAAAAGAAGGCTCATTGCCACCATGCGGAGCAAGCCGTGGCCCATGGCGAAGAAG 555

Qy 181 LeuThrGluLeuArgGlnValGlnAspPheValGlyLysTyrGluGlyAlaLeuGluLys 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 556 CTGACAGAGCTCAGGGAGGCCCAGGAAGTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAG 615

Qy 201 GlyLysGlyGlyGlnLeuThrTyrAlaTyrLysLysMetLeuMetAlaLysLysLysTrpPhe 220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 616 GGGAAAGGCAGCCAACTATATCCCTAACAAGATGCTGATGGCCAAGAAAATGGGTCAAATTT 675

Qy 221 LysArgAspPheAspAspAsnPheLysThrGlnCysIleProTrpGluMetLysIleLysAsp 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 676 AAGAGAGACTTTGATAATTTGAAGACTCAAATGTATCCCCTGGAAATGAAGATCAAGGAC 735

Qy 241 IleGluSerHisSerPheLysSerSerValAlaSerTyrPheIlePheLeuArgTrpMetTyr 260
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Db 736 ATTGAAAGTCACTTTGGTTCTTCAGTGGCATCAGTATTTCATCTTTCTCCGATGGATGTAT 795

Qy 261 GlyValAsnLeuValLeuPheGlyLeuIlePheLeuValIleIleProGluValLeu 280
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Db 796 GGAGTTAACCTTGTCCTTTTGGCTTAATTATTTGGTCATTATTATAATCCCAGAGGTACTG 855

Qy 281 MetGlyMetProTyrGlySerIleProArgArgLysThrValProArgArgAlaGluArgLys 300
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Db 856 ATGGGCATGCCCTATGGGAGTATTCCCAGAAGACAGTGCCTCGGGCTGAGGAAGAAAAG 915

Qy 301 AlaMetAspPheSerValLeuTrpAspPheGluGlyTyrIleLysTyrSerAlaLeuPhe 320

Db   916 GCCATGGATTTTCTTGTCTTTGGGATTTGAGGGCTATATCAAGTACTCCACTCTTC 975
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Qy   321 TyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTrpLeuArgTyrArgLeuProMetAla 340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   976 TATGGCTACTACAACAACCAGAGACCAATCGGGTTGGCTGGGCTACCGGCTGCCTATGGCT 1035
Qy   341 TyrPheMetValGlyValSerValPheGlyTyrSerLeuIleIleValIleArgSerMet 360
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Db   1036 TACTTTATGGTGGGGGTCAGGGTGTTCGGCTACAGCCTGATTATTGTCATTCGAAGTATG 1095
Qy   361 AlaSerAsnThrGlnGlySerThrGlyGluGlyGluSerAspAsnPheThrPheSerPhe 380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 GCCAGCAATACCCAAGGAAGCACAGGGGAGGGAGAGTCAGACAACTTCACATTCAGCTTC 1155
Qy   381 LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr 400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 AAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATAACAAATAT 1215
Qy   401 AlaSerIleThrThrSerPheLeuSerGluSerIleValAspGluGlnSerAsnLysGlu 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAGAGTAACAAAGAA 1275
Qy   421 GluAsnIleHisLeuThrArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysCys 440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 GAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGT 1335
Qy   441 LeuCysGlySerGlyTyrLeuIleGlyTyrPheValValLysArgSerGlnGlnPheSerLys 460
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Db   1336 TTGTGTGGAAGTGGGTACCTCATTACTTTGTGGTTAAGCGATCTCAGCAATTCTCCAAA 1395
Qy   461 MetGlnAsnValSerTrpTrpGluArgGluAsnGluValIleValMetSerLeuLeuGly 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 ATGCAGAATGTCAGCTGGTGGGAAAGGGAAAATGAGGTAAGGATCGTGATGTCCCTGCTTGGA 1455
Qy   481 MetPheCysProProLeuPheGluThrIleAlaAlaLeuGluGlyAsnTyrHisProArgThr 500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 ATGTTTTGTCCCCCTCTGTTTGAAACCATCGCTGCCCTGGAGGGAAATTACCACCCACGGACT 1515
Qy   501 GlyLeuLysTrpGlnLeuGlyArgIlePheAlaLeuPheLeuGlyAsnLeuTyrThrPhe 520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 GGACTGAAGTGGCAGCTGGGCAGGATCTTTGCACTCTTCCTGGGGAACCTCTACACATTT 1575
Qy   521 LeuLeuAlaLeuMetAspAspValHisLeuLysLeuAlaAsnGluGlnThrIleLysAsn 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 CTCTTGGCCCTGATGGATGACGTCCACCTCAAGCTTGCTAATGAACAATAAAGAAC 1635
Qy   541 IleThrHisTrpThrLeuPheAsnTyrTyrAsnSerSerGlyTyrPheAsnGluSerValPro 560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 ATCACTCACTGGACTCTGTTTAACTATTACAACTCCTCTGGTTGGACGAGAGTGTCCCC 1695
Qy   561 ArgProProLeuHisProAlaAspValProArgGlySerCysTrpLeuGlyThrSerAsnSerAla 580
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Db   1696 CGACCACCCCTGCACCCTGCAGATGTCCCCGGGGTTCTGCTGGACACTCAAATTCTGCC 1755
Qy   581 IleGluPheMetArgLeuThrValSerAspMetLeuValThrTyrIleThrIleLeuLeu 600
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Db

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Qy   601 GlyAspPheLeuArgAlaCysSerPheValGluAlaArgPheMetAsnTyrCysTrpAspTrpLeu 620
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Db   1816 GGGGACTTCCTACGGGCTTGTTTTGTGGGGTTCAGTGAACTACTGCTGGTTGGGACTTG 1875
Qy   621 GluAlaGlyPheProSerTyrAlaGluPheAspIleSerGlyAsnValValLeuGlyIle 640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 GAGGCTGGATTTCCTTCATATGCTGAGTTTGATATTAGTGGAAATGTGGTTTGATC 1935
Qy   641 PheAsnGlyGlyMetIleTrpPheGlyTyrAlaProGlyLeuValGlyIleAsn 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TTCAACGGAGGAATGATCTGGATGGGCTCCTTCCATGCTCCAGGCCTGGTGGGCATTAAT 1995
Qy   661 ValLeuArgLeuLeuThrSerMetTyrPheGlnCysTrpLeuaValMetSerSerAsnVal 680
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Db   1996 GTGCTGCGCCTGCTGACTCCANGTACTTCCAGTGCTGGCTGGGCGTGATGAGCAGCAACGTA 2055
Qy   681 ProHisGluArgValPheLysAlaSerArgSerAsnAsnPheTyrMetCysGlyLeuLeuLeu 700
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Db   2056 CCCCATGAACGCGTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGTGCGGCCTGCTG 2115
Qy   701 LeuValLeuPheLeuSerLeuProValAlaTyrThrIleMetSerLeuProProGlu 720
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Db   2116 CTGGTGCTCTTCCTCAGCCTCCCGGTGGCCTACACCATCATGTCCCTGCCACCCTCC 2175
Qy   721 PheAspCysGlyProPheSerGlyLysAsnArgMetTyrAspValLeuGlnGluThrIle 740
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Db   2176 TTTGACTGCGGCCCGTTCAGTGGGAAAAACAGAATGTACGATGTCCTCCAAGAGACCATT 2235
Qy   741 GluAsnAspPheProThrPheLeuGlyLysIlePheAlaPheLeuAlaAsnProGlyLeu 760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 GAAAACGATTTCCCAACCTTCCTGGGCAAGATCTTTGCTTTCCTCGCCAATCCAGGCCTG 2295
Qy   761 IleIleProAlaIleAlaLeuLeuMetPheLeuaValAlaIleTyrTyrLeuAsnSerValSerLys 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 ATCATCCCAGCCATCGCTGCTGATGTTCTTGGCCATTTACTACCTGAACTCAGTTTCCAAA 2355
Qy   781 SerLeuSerArgLeuAsnAlaGlnLeuArgLysTyrIleGlnValLeuLeuArgGlyValGlu 800
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Db   2356 AGCCTTTCCCGAGCTAATGCCCAGCTGAGGAAGAAAATCCAAGTGCTCCGTGAAGTTGAG 2415
Qy   801 LysSerHisLysSerValLysGlyLysLysIleLysLysAspSerThrProLys 820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 AAGAGTCACAAATCTGTAAAAGGAAAGAAGATCAAGAAGGACAGCACCCCTAA 2475
Qy   821 SerSerSerLysAsnAlaThrGlnLeuGlnLeuThrLysGluGlnThrThrProSer 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476 AGGAGCTCCAAAAATGCCACCCAGCTCCAACTCACCAAGGAGCAGACCACTCCCTCT 2535
Qy   841 AlaSerGlnSerGlnAlaMetAspLysLysLysAlaGlnIleGlyTyrSerAsnSerAla 860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 GCCAGCCAAAGCCAGGCCATGGACAAGAAGAAGGCGCCGGGGACTTCCAAATTCTGCC 2595
Qy   861 SerArgThrThrLeuProAlaSerGlyHisLeuProIleSerSerArgProProGlyIleIleGly 880
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Db   2596 ACCAGGACCACACTGCCTGCCTCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGA 2655

RESULT 2
US-10-487-887-3
; Sequence 3, Application US/10487887
; Publication No. US2004024913A1
; GENERAL INFORMATION:
; APPLICANT: Griffith, Andrew J
; APPLICANT: Kurima, Kiyoto
; APPLICANT: Wilcox, Edward
; APPLICANT: Friedman, Thomas
; TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO
HEREDITARY
; TITLE OF INVENTION: DEAFNESS
; FILE REFERENCE: 226544
; CURRENT APPLICATION NUMBER: US/10/487,887
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US02/29614
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/323,275
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 3121
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-887-3

Alignment Scores:
Pred. No.:
Score: 0   Length: 3121
Percent Similarity: 879.00   Matches: 879
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 97.02%   Indels: 0
                                    8   Gaps: 0

US-10-792-307-4 (1-906) x US-10-487-887-3 (1-3121)

Qy   28 GlyAspAargLeuGlyArgArgSerSerLysArgAlaLeuLysAlaGlyThrPro 47
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Db   88 ArgGlyGluAlaGluArgThrCysGlyGlyArgArgLysArgArgAspGluAlaSerGlyPhe 107
Db   88 ArgGlyGluAlaGluArgThrCysGlyGlyArgArgLysArgArgAspGluAlaSerGlyPhe 107

Qy   49 GGTGACAGGCTGGGAAGGAGAATCCTCAAGCAACGCGGCGCCTCAAAGCCGAGGGGACCCCA 108
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Db 229 CGGGGGCGAGGGCAGGAGAGGAGAGACCTGCCAGCGAGGCAGGAGAGAAAGCGGGACCGAGAGGGGCCTCCTTC 288

Qy 108 GlnGluArgThrAlaAlaProLysAlaGlyLysIleProArgLysGluGluLysSer 127
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Qy   48 GlyArgArgGlyAlaGluGlnArgSerGlnLysGluArgAlaGlyGlySerProSerProGly 67
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Db 289 CAGGAGCGGACAGCAGCGCCCAAAGAGGGGAAAAGGAGAATTCCGAGGAAGGAGGAAGTCG 348

Qy 108 AlaGlnArgProHis 906
         ||||||||||||
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Qy 128 LysArgGlnLysGlyProArgSerSerLeuAlaSerSerAlaSerGlyGlyGluSer 147
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Db 349 AAGCGGCAGAAGAGAAAACCAGGTCATCCTCCTTGGCCTCCAGTGCCTTGGTGGGGGAGTCC 408

Qy 148 LeuSerGluGluGluLeuAlaGlnIleLeuGlnLnValGluGluGluLysLeuIle 167
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 409 CTGTCCGAGGAGGAACTGGCCCAGATCCTGCAGGTGGAGGAAGAAAAGCTCATT 468

Qy 168 AlaThrMetAlaGlnSerLysProTrpProMetAlaAlaLysLysLeuThrGluLeuArgGluAla 187
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Db 469 GCCACAATGGCCCAGAGCAAGCCCTGGCCCATGGCGGCGAAGAAGCTGACAGAGCTCAGGGAGGCC 528

Qy 188 GlnGluPheValGlyLysThrGluGlyValAlaLeuGlyLysLysGlyLysLeuLeuTyr 207
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Db 529 CAGGAATTTGTGGGAGAAGTATGAAGGTGCCTTGGGAAAGGGAAAAGGGAAGAACTATAT 588

Qy 208 AlaTyrLysMetLeuMetAlaLysLysTrpIleValLysLysPheLysAspAspAsnPhe 227
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Db 589 GCCTACAAGATGCTGATGGCCAAGAAATGGGTCAAATTAAGGAAGAACTTTGATAATTTC 648

Qy 228 LysThrGlnCysIleProTrpGluMetLysLysAspAspIleGluSerHisPheGlySer 247
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Db 649 AAGACTCAATGTATCCCCTGGGAAATGAAGATCAAGGACATTGAAAGTCACTTTGGTTCT 708

Qy 248 SerValAlaSerTyrPheIlePheHisLeuArgTrpMetTyrGlyValAlaSnLeuValLeuPhe 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 709 TCAGTGGCATCGTATTTCATCTTTCCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTT 768

Qy 268 GlyLeuIlePheGlyValIleIleProGluValLeuMetGlyMetProTyrGlySer 287
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 769 GGCTTAATATTTGGTCTAGTCATAATCCCAGAGGTACTGATGGGCATGCCCTATGGGAGT 828

Qy 288 IleProArgGlyThrValProArgAlaGluGluGluGluLysAlaMetAspPheSerValLeu 307
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 829 ATTCCCAGAAGAGCAGTGCCTCGGGCTGAGGAAGAAAAAGGCCATGGATTTTCTGTCCTT 888

Qy 308 TrpAspPheGluGlyTyrIleGlyTyrGlyTyrTyrTyrAsnAsnGln 327
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Db 889 TGGGATTTTGAGGGCTATATCAAGTACTACTGCTACTACAACAACCAG 948

Qy 328 ArgThrIleGlyTyrTrpLeuArgGlyLeuProMetAlaTyrPheMetValGlyValSer 347
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Db 949 AGGACAATCGGGTGGCTGAGGTACCGGCTGCCTATGGCTTACTTTATGGTGGGGGTCAGC 1008

Qy 348 ValPheGlyTyrSerLeuIleIleValIleIleAlaSerMetAlaSerAsnThrGlnGlySer 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169 TCTCCCCGGAGGAAGGAAAACAGGGCCGCAGGAGGAGACACAGAGAAAGAGCTGGGGGAGCAGGAG 228
Db 1009 GTGTTCGGCTACAGCCTCATTATTGTCATTGCCAGCATGGCCAGCAATACCCAAGGGAAGC 1068

Qy   68 SerProArgArgLysGlnThrGlyArgArgHisArgGluGluLeuGlyGlnGlu 87
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 169 TCTCCCCGGAGGAAGGAAAACAGGGCCGCAGGAGGAGACACAGAGAAAGAGCTGGGGGAGCAGGAG 228

Qy   368 ThrGlyGluGlySerAspAsnPheThrPheSerPheLysMetPheThrSerTrpAsp 387
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Db   1069 ACAGGCGAAGGGAGAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGAC 1128

Qy   388 TyrLeuIleGlyAsnSerGlyThrAlaAspAsnLysTyrAlaSerIleThrThrSerPhe 407
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 TACCTGATCGGGAATTCAGAGACAGCTGATAACAAAATATGCATCCATCACCACCAGCTTC 1188

Qy   408 LysGluSerIleValAlaAspGluGlnLysGluSerAsnLysGluGluAsnIleHisLeuThrArg 427
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1189 AAGGAAATCAATAGTGAGTGAAGAACAGAAAGAGTAACAAAGAGAAAATATCATCTGACAAGA 1248

Qy   428 PheLeuArgValAlaLeuAlaAsnPheLeuIleIleCysGlySerLeuCysGlySerGlyTyrLeu 447
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 TTCTTCGTGTCCTGGCCAACTTTCTACATCATCTGCGTTTGTGTGGAAGTGGGTACCTC 1308

Qy   448 IleTyrPheValValLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrpTyr 467
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 ATTTACTTTGTGGTTAAGCCGATCTCAGCCAATTCTCCAAAATGCAGAATGTCAGCTGGTAT 1368

Qy   468 GluArgAsnGluValGlnIleIleValMetSerLeuLeuGlyMetPheCysProCysProLeuPhe 487
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 GAAAGGAAATGAGGTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCTCGTTT 1428

Qy   488 GluThrIleAlaLeuAlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGly 507
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 GAAACCATCGCTCGCCTGACGAATTACCACACCAGGACTGGACTGAAGTGGCAGCTGGGA 1488

Qy   508 ArgIlePheLeuLeuPheLeuGlyAsnLeuTyrThrPhePheLeuAlaLeuMetAspAsp 527
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 CGGATCTTTCCACTCTTTCCTGGGAACCTCTACACATTCTTTCTTGGCCCTGATGGATGAC 1548

Qy   528 ValHisLeuLysLeuAlaAsnGluGluThrIleLysAsnIleThrHisTrpThrLeuPhe 547
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 GTCCACCTCAAGCTTCCTAATGAAGAGACAATAAAGAACATCACTCACTGGACTCTGTTT 1608

Qy   548 AsnTyrTyrAsnSerGlyTrpAsnGluSerValProArgProLeuHisProAla 567
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 AACTATTACAACTCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACACCCTGCACCCTGCA 1668

Qy   568 AspValProArgGlySerCysTrpGluThrAlaValGlyTyrIleGluPheMetArgLeuThr 587
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 GATGTCCCCCGGGGGTTCTTGCGTGGGACAGCTGTGGGATACATTGAATTCATGAGGCTGACG 1728

Qy   588 ValSerAspMetLeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAlaCys 607
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 GTGTCTGACATGCTGGTAACGTACATCACCATCCTGCTGGGGGACTTCCTACGGGCTTGT 1788

Qy   608 PheValArgPheMetAsnTyrCysTrpTrpTrpPheAsnGlnGlyMetIleTrp 647
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 TTTGTGCGGTTCATGAACTACTGCTGGTGGTGGTTCGGGAGCTTGGAGGCTGGAGTTCATATAT 1848

Qy   628 AlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrp 647
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 GCTGAGTTTGATATTAGTGGAAATGTCCTGGGTTTGATCTTCAACCAAGGAATGATCTGG 1908

Qy   648 MetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeuLeuThrSer 667
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 ATGGGCCTCCTTCTTATGCTCCAGCGCTGTGGTGGGCATTAATGTGCTGCGGCTGCTGACCTCC 1968

Qy   668 MetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArgValPheLys 687
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 ATGTACTTCCAGTGCTGGGCCGTGATGAGCAGCAATGTCCCCCATGAACGGGTGTTCAAA 2028

Qy   688 AlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPheLeuSerLeu 707
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 GCCTCCCGATCCAACAACTTCTACATGGGCCTTCTGCTCCTGGTGCTCTTCCTCAGCCTC 2088

Qy   708 LeuProValAlaTyrThrIleMetSerLeuProSerPheAspCysGlyProPheSer 727
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 CTGCCGGTGGCCTACACCATCATGTCCCTGCCCAGCTTTGACTGCGGGCCGTTCAGT 2148

Qy   728 GlyAsnAsnArgMetTyrAspValLeuGlyGluGlnThrIleGluAsnAspPheProThrPhe 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 GGGAAACACAGAATGTACGATGTCCTCGGAGAGCAGACCATTGAAAACGATTTCCCAACCTTC 2208

Qy   748 LeuGlyLysIlePheAlaAlaAlaAsnProGlyLysIleLeuIleLeuAlaIleLeuLeu 767
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 CTGGGCAAGATCTTTGCTGCTGCCAATCCAGGCAAGATCCTGATCCTAGCCATCCTGCTG 2268

Qy   768 MetPheLeuAlaIleTyrTyrTyrLeuAsnSerValSerLeuSerArgAlaAlaAsnAla 787
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 ATGTTCTTGGCCATTTACTACTATCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAATGCC 2328

Qy   788 GlnLeuArgLysLysLeuGlnValValGluGluSerHisLysSerValVal 807
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 CAGCTGAGGAAGAAAAATCCAAGTCACCTCCGTGAAGTTGAGAGAGTCACAAAATCGTAAAA 2388

Qy   808 GlyLysAlaThrAlaArgAspAspSerGluAspSerSerSerLysAspAsnAlaThr 827
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 GGCAAAGCCACAGCCAGAGATGCGAGGAGACACAACTAAAAGCAGCTCCAAAAATGCCACC 2448

Qy   828 GlnLeuGlnLeuThrGlnThrThrProProSerAlaSerGlnSerGlnAlaMet 847
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 CAGCTCCAACTCACACAAGGAGAAGACACACTCCTCCCTCTGCCCAGCGAAGCCAGCCATG 2508

Qy   848 AspLysLysAlaGlnGlyProGlyThrGlyProGlyProSerAlaSerGlnSerGlnThrLeuProAla 867
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 GACAAGAAGGCGCCAGGGCCCTGGAACTCCAATTCTGCAGGAACCACACTGCCTGCC 2568

Qy   868 SerGlyHisLeuProIleSerSerArgProProGlyIleGlyProAspSerGlyHisIleAlaPro 887
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 TCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGAACCAGATTCTGGCCACATCGCCCCA 2628

Qy   888 SerGlnThrHisProTrpArgSerAlaSerGlyGlySerAlaGlnAsnArgProProHis 906
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 TCTCAGACTCATCCGTGGAGGTCAGCGGGTGGCTCAGCAGCAGAGAACCTCCCCAC 2685

RESULT 3
US-10-115-831-134
; Sequence 134, Application US/10115831
; Publication No. US20030219743A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom

Alignment Scores:

Pred. No.:
Score: 0
Percent Similarity: 583.00
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 64.35%

Length: 4895
Matches: 583
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-792-307-4 (1-906) x US-10-115-831-134 (1-4895)

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Qy    312 GlyTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGly 331
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Db   1096 GGCTATATCAAGTACTTCGCACTCTTCTATGGCTACTACAACAACCAGAGGACCATCGGG 1155

Qy    332 TrpLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyr 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 TGGCTGAGGTACCGGCTGCCTATGGCTTACTTTATGGTGGGGGTCAGCGTGTTCGGCTAC 1215

Qy    352 SerLeuIleIleValIleArgSerMetAlaSerArgAsnThrGlnGlySerThrGlyGlu 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 AGCCTGATTATTGTCATTCGATCGATGGCCAGCAATACCCAAGGAAGCACAGGGAGGAAGG 1275

Qy    372 GluSerAspAsnPheThrPheSerPheLysMetPheThrSerPheLysIleLeuIleGly 391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 GAGAGTGACAAGTTCACATTCAGCTTCAAGATGTTCACCAGCTTCAAGATACTCATCGGG 1335

Qy    392 AsnSerGluThrAlaAspAsnLysTyrAlaSerIleThrThrSerPheLysGluSerIle 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 AATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATA 1395

Qy    412 ValAspGluGlnGlnSerAsnLysGluGlnAsnIleHisLeuThrArgPheLeuArgVal 431
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 GTGGATGAACAAGAGAGTAACAAAGAGAAAAATCATCTGACAAGGATTTCTTCGTGTC 1455

Qy    432 LeuAlaAsnPheLeuIleIleCysCysLeuCysGlySerGlyTyrLeuIleTyrPheVal 451
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 CTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTCATTTACTTTGTG 1515

Qy    452 ValLysArgSerGlnGlnPheSerGlyLysMetGlnAsnValSerTrpTyrGluArgAsnGlu 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 GTTAAGCGATCTCAGCAATTCTCCAAAATGCAAAATGTCAGCTGGTATGAGAAGAATGAG 1575

Qy    472 ValGluIleValMetSerLeuLeuGlyMetPheCysProProLeuPheGluThrIleAla 491
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 GTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCCTCTGTTTGAAACCATCGCT 1635

Qy    492 AlaLeuGluAsnTyrHisProArgThrGlyLeuGlyTrpGlnLeuGlyArgIlePheAla 511
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GCCCTGGAGAATTACCACCCCAGGACACTGGACTGGAGTGCAGCTGGGACCGCAATCTTTGCA 1695

Qy    512 LeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAspValHisLeuLys 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 CTCTTCCTGGGGAACCTCTACACATTTCTTCTTGCCCTGATGGATGATGTCCACCTCAAG 1755

Qy    532 LeuAlaAsnGluGluThrIleLysAsnIleThrHisTrpThrLeuPheAsnTyrTyrAsn 551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 CTTGCTAATGAAGAGACAATAAAGAACATCACTCACTGGACTCTGTTTAACTATTACAAC 1815

Qy    552 SerSerGlyTrpAspAsnGluSerValProArgProProLeuHisProAlaAspValProArg 571
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 TCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCAGATGTGCCCCGG 1875

Qy    572 GlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeuThrValSerAspMet 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 GGTTCTTGCTGGGAGACAGCTGTGGGCATTGAATTCATGAGGCTGACGGTGTCTGACATG 1935

Qy    592 LeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAlaCysPheValArgPhe 611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 CTGGTAACGTACATCACAATCCTGCTGGGGGACTTCCTACGGGCGTGTTTTGTGCGGTTC 1995

Qy    612 MetAsnTyrCysTrpCysTrpAspLeuGluAlaGlyPheProSerTyrAlaGluPheAsp 631
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Db   1996 ATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGGATTCCCTATATGCTGAGTTTGAT 2055

Qy    632 IleSerGlyAsnValLeuGlyLeuPheAsnGlnGlyMetIleTrpMetGlySerPhe 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 ATTAGTGGAAATGTCCTGGGTTTGATCTTCAACCAAGGAATGATCTGGATGGGCTCCTTC 2115

Qy    652 TyrAlaProGlyLeuValGlyIleAlaAsnValLeuLeuThrSerMetTyrPheGln 671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 TATGCTCCAGGCCTGGTGGGCATTAATGTGCTGCGCAACTCCATGTACTTCCAG 2175

Qy    672 CysTrpAlaValMetSerSerAsnValProHisGluArgValPheLysValAlaSerArgSer 691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 TGCTGGGCCGTGATGAGCAGCAACGTACCCCATGAACGGGTCTTCAAAGGCCTCCGAATCC 2235

Qy    692 AsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPheLeuSerLeuLeuProValAla 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AACAACTTCTACATGGGGCTCCTGCTGCTGGTGCTCTTCCTCAGCCTGCTGCCGGTGGCC 2295
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; SOFTWARE: Custom
; SEQ ID NO 28100
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1906)..(2340)
; OTHER INFORMATION: 100% homologous to Homo sapiens dJ686C3.3 (novel
; OTHER INFORMATION: gene), accession number AL049712, Smith-Waterman Score=778.
US-10-450-763-28100

Alignment Scores:
Pred. No.:
Score: 583.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 64.35%

Length:	5027
Matches:	583
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-792-307-4 (1-906) x US-10-450-763-28100 (1-5027)

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Qy  312 GlyThrTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGly 331
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1096 GGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACAACAACCAGAGGACCATCGGG 1155

Qy  332 TrpLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyr 351
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1156 TGGCTGAGGTACCGGCTGCCTATGGCTTACTTTATGGTGGGGGTCAGCGTGTTCGGCTAC 1215

Qy  352 SerLeuIleIleValIleLeuArgSerMetAlaSerAsnThrGlnIleGlySerThrGlyGly 371
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1216 AGCCTGATTATTGTCATTCGATCGATGGCCAATACCCAAGGAGACAGGGTGGGGAAGGG 1275

Qy  372 GluSerAspAsnPheThrPheSerPheLysMetPheThrSerTrpAspTyrLeuIleGly 391
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1276 GAGAGTGACAACTTCACATTCAGCTTCAAGATGTTCACCAGCTGGGACTACCTGATCGGG 1335

Qy  392 AsnSerGluThrAlaAspAsnLysTyrAlaSerIleIleThrThrSerPheLysGluSerIle 411
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1336 AATTCAGAGACAGCTGATAACAAATATGCATCCATCACCACCAGCTTCAAGGAATCAATA 1395

Qy  412 ValAspGluGlnLeuSerAsnLysGluGluAsnIleHisLeuThrArgPheLeuArgVal 431
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1396 GTGGATGAACAAGAGAGTAACAAAGAGAAAAATATCCATCTGACACAGAGATTCCTGCGTGTC 1455

Qy  432 LeuLeuAsnPheLeuIleIleCysGlyCysLeuCysGlySerGlyTyrTyrLeuIleTyrPheVal 451
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Db 1456 CTGGCCAACTTTCTCATCATCTGCGGCTGTCTTTGTGGAAGTGGGTACCTCATTTACTTTGTG 1515

Qy  452 ValLysArgSerGlnPheSerLysMetGlnAsnValSerTrpTyrGluArgAsnGlu 471
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Db 1516 GTTAAGCGGATCTCAGCCAATTCTCCAAAATGCAGAATGTCAGCTGGTATGAAAGGAATGAG 1575

Qy  472 ValGluIleValMetSerLeuLeuGlyMetPheCysProProLeuPheGluThrIleAla 491
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Db 1576 GTAGAGATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCCTCTGTTTGAAACCATCGCT 1635
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Qy  712 TyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSerGlyLysAsnArg 731
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Db 2296 TACACCATCATGTCCCTCCACCCTCCTTTGACTGCGGGCCGTTCAGTGGGGAAAAACAGA 2355

Qy  732 MetTyrAspValLeuGlnGluThrIleGlyAspAsnAspPheProThrPheLeuGlyIleIle 751
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Db 2356 ATGTACGATGTCCTCCAAGAGACCATTGGAAAACCATTTCCAACCTTCCTGGGCAAGATC 2415

Qy  752 PheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleLeuLeuMetPheLeuAla 771
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Db 2416 TTTGCTTTCCTGGCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTGATGTTCTTGGCC 2475

Qy  772 IleThrTyrTyrLeuAsnSerValSerLysSerLeuSerArgAlaAsnAlaGlnLeuArgLys 791
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Db 2476 ATTTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCAGACTAATGCCACCTGAGGAAG 2535

Qy  792 LysIleGlnValLeuArgGluValGluHisSerHisLysSerValLysGlyLysAlaThr 811
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Db 2536 AAAATCCAAGTGCTCCGTGAAGTTGAGAGAGCCCACAAAATCTGTAAAAGGCAAAGCCACA 2595

Qy  812 AlaArgAspSerGluAspThrProLysSerSerSerLysAsnAlaThrGlnLeuGlnLeu 831
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Db 2596 GCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCTCCAACTC 2655

Qy  832 ThrLysGlyLeuThrThrProProSerAlaSerGlnAlaSerGlnAlaMetAspLysAla 851
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2656 ACCAAGGAAGGACCACTCCTCCCTCCTGCCAGCCAAGCCAGTCCATGGACAAGGCG 2715

Qy  852 GlnGlyProGlyThrSerAsnSerAlaSerArgThrThrLeuProAlaSerGlyHisLeu 871
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2716 CAGGGCCCTGGGACCTCCAATTCTGCCAGCAGGACCACACTGCCTGCCTCTGGACACTT 2775

Qy  872 ProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaProSerGlnThrHis 891
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2776 CCTATATCTCGGCCCCCTGGAATCGGACCAGATTCTGGCCACGCCCCCATCTCAGACTCAT 2835

Qy  892 ProTrpArg 894
        |||||||
Db 2836 CCGTGAGA 2844
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Qy    492  AlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGlyLysArgIlePheAla  511
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Db   1636  GCCCTGGAGAATTACCACCCGACTGGACTGAAGTGGCAGCTGGGACGCGGATCTTTGCA     1695

Qy    512  LeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAspValHisLeuLys     531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696  CTCTTCCTGGGGAACCTCTACACATTTCTTGGCCCTGATGAGGTCCACCTCAAG          1755

Qy    532  LeuAlaAsnGluGluThrIleLeuTyrAsnIleThrHisTrpLeuPheAsnTyrTyrAsn    551
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756  CTTGCTAATGAAGAGCAAATAAAGAACACTCACTGGACTCTGTTTAACTACTATAACAAC    1815

Qy    552  SerSerGlyTrpAsnGluSerValProArgProProLeuHisProLeuAlaAspValProArg  571
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816  TCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCAGATGTCCCCGG     1875

Qy    572  GlySerCysTrpGluThrAlaValAlaValGlyIleGluPheMetArgLeuThrValSerAspMet  591
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876  GGTTCTTGCTGGGAGACAGCTGTGGCAGTTGGGATTGAGTTCATGAGGCTGACGGTGTCTGACATG  1935

Qy    592  LeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuuArgAlaCysPheValArgPhe    611
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936  CTGGTAACGTACATCACCATCCTCGGGGACTTCCTACGGGCTTGTTTTGTGCGGTTC       1995

Qy    612  MetAsnTyrCysTrpTrpAspLeuGluLeuAlaGlyPhePheProSerTyrAlaGluPheAsp   631
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996  ATGAACTACTGCTGGTGGGACTTGGAGCTGGCAGGCTTCTTCCCTTCATATGCTGAGTTTGAT  2055

Qy    632  IleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrpMetGlySerPhe     651
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056  ATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAGGAATGATCTGGATGGGCTCCTTC     2115

Qy    652  TyrAlaProGlyLeuValGlyIleLeuAsnValLeuArgLeuLeuThrSerMetTyrPheGln   671
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116  TATGCTCCAGGCCTGGTGGGCATTAATGTCCTGCGGCTCCTGACCTCCATGTACTTCCAG    2175

Qy    672  CysTrpAlaValPheLeuLysSerAsnValProHisGluArgValPheLysAlaSerArgSer   691
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176  TGCTGGGCGGTGATGACACGAGCAAGCGTACCCCATGAACGGGTGTTCAAAGCCTCCGATCC   2235

Qy    692  AsnAsnPheTyrMetGlyLeuLeuValLeuPheLeuSerSerLeuProValAla          711
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236  AACAACTTCTACATGGGCCTCCTGCTGCTTCCTCAGCCTCCTGCCGGTGGCC           2295

Qy    712  TyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSerGlyGlyAsnArg    731
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296  TACACCATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGTGGGAAAAACAGA    2355

Qy    732  MetTyrAspValValLeuGlnThrIleGluAsnAspPheProThrPheLeuGlyLysIle    751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356  ATGTACGATGTCCTCCAAGAGACCATTGAAAACGATTTCCCAACCTTCCTGGGCAAGATC    2415

Qy    752  PheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleIleLeuLeuMetPheLeuAla   771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416  TTTGCTTTCCTGGCCAATCCAGGCCTGATCATCCCAGCCATCTGCTGATGTTCTTGGCC    2475
```

```
Qy    772  IleTyrTyrTyrLeuAsnSerValSerArgLysSerLeuSerArgArgAlaAsnAlaGlnLeuLeuArgLys  791
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476  ATTTACTACTACCTGAACTCAGTTTCCAAAAGCCTTTCCCGAGCTAAATGCCCAGCTGAGGAAG          2535

Qy    792  LysIleGlnValLeuArgGluLysLysSerHisLysSerValLysGlyLysAlaThr       811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536  AAAATCCAAGTGCTCCGTGAAGTTGAGAAGAGTCACAAATCTGTAAAAGGCAAAGCCACA    2595

Qy    812  AlaArgAspSerGluAspThrProLysSerSerSerGlyAsnAlaThrGlnLeuGlnLeu    831
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596  GCCAGAGATTCAGAGGACACACCTAAAAGCAGCTCCAAAAATGCCACCCAGCTCCAACTC    2655

Qy    832  ThrLysGluGluThrThrProProSerAlaSerGlnAsnLeuMetAspLysLysAla      851
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2656  ACCAAGGAAGAAGACCACTCCCCTCCTGCCAGCCAGAACCAGCCCATGGACAAGAAGGCG    2715

Qy    852  GlnGlyProGlyThrSerAsnSerAlaSerArgThrLeuProAlaSerGlyHisLeu      871
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2716  CAGGGCCCTGGGACCTCCAATTCTGCAAGCAGGACACTGCCTGCCTCTGGACACCTT      2775

Qy    872  ProIleSerArgProProGlyValIleGlyProAspSerGlyHisAlaProSerGlnThrHis  891
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776  CCTATATCTCGGCCCCCTGGAATCGGACCAGATTCGGCGACCCCCATCTCAGACTCAT     2835

Qy    892  ProTrpProArg  894
           ||||||||
Db   2836  CCGTGGAGA    2844
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Alignment Scores:

Pred. No.:		Length:	2560
Score:	1.62e-188	Matches:	2560
	198.00	Matches:	198
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	21.85%	Indels:	0
DB:	6	Gaps:	0

US-10-792-307-4 (1-906) x US-10-108-260A-342 (1-2560)

```
Qy    427  ArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysGlyLeuCysGlySerGlyTyr   446
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;   PRIOR FILING DATE: 2001-09-19
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 7
;   LENGTH: 3216
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-487-887-7

Alignment Scores:
Pred. No.:              1.426e-88    Length:         3216
Score:                  99.00        Matches:        140
Percent Similarity:     98.59%       Conservative:   0
Best Local Similarity:  98.59%       Mismatches:     1
Query Match:            10.938       Indels:         2
DB:                     8            Gaps:           0

US-10-792-307-4 (1-906) x US-10-487-887-7 (1-3216)

Qy   213  MetAlaLysLysTrpValLysPheLysArgAspPheAsnPheLysThrGlnCysIle  232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904  ATGGCTAAGAAAATGGGTCAAGTTCAAGAGGGGACTTTGATAATTTCAAGACTCAATGTATT  963

Qy   233  ProTrpGluMetLysIleLysLysAspIleGluSerHisPheGlySerSerValAlaSerTyr  252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964  CCCTGGGAAATGAAGATCAAGAAAGACATTGAAAGTCACTCGGGTTCTTCTGTGGCATCTTAC  1023

Qy   253  PheGluPheLeuArgTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly  272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024  TTCATCTTTCTCCGATGATGTATGGAGTTAACCTTGTCCTTTTTGGCTTAATATTTGGT  1083

Qy   273  LeuValIleIleProGluValLeuMetGlyMetProTyrGlySerIleProArgLysThr  292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1084  CTAGTCATCATCCCAGAGGTGCTGATGGGCATGCCCTATGGAAGTATACCCAGAAAGACG  1143

Qy   293  ValProArgAlaGluGluGlyLys-AlaMetAspPheSerValLeuTrpAspPheGluGl  312
          ||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db  1144  GTGCCTCGAGCTGAGGAAGGAGCG-AGCCATGGACTTCTCTGTCCTTTGGGATTTTGAGGG  1202

Qy   312  yTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyr  332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1203  CTACATCAAAATATTCTGCTCTCTTCTACTGGCTACTACAACAACCAGCGGACCATTGGATG  1262

Qy   332  pLeuArgTyrArgLeuProMetGluTyrPheMetValGlyValSerValPheGlyTyrSe  352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1263  GCTGAGGTACAGGCTGCCCATGGCTTACTTTATGGTGGGGGTCAGGGTGTTGGCTACAG  1322

Qy   352  rLeu  353
          ||||
Db  1323  CTTG  1326
```

RESULT 7
US-10-792-307-7
;   Sequence 7, Application US/10792307
;   Publication No. US20050196759A1
;   GENERAL INFORMATION:
;   APPLICANT: Griffith, Andrew J.

```
Db     2  AGATTTCTTCGTCGTCCTGGCCACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTAC  61

Qy   447  LeuIleTyrPheValValLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrp  466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    62  CTCATTTACTTTGTGGTTAAGCGATCTCAGCAATTCTCCAAAATGCAGAATGTCAGCTGG  121

Qy   467  TyrGluArgAsnGluValGlyIleGluValMetSerIleLeuGlyMetPheCysProLeu  486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122  TATGAAAGGAATGAGGTAGAGATCGTGATGTCCCTTGCTTGGAATGTTTTGTCCCCTCTG  181

Qy   487  PheGluThrIleAlaAlaLeuGlyAsnTyrHisProArgThrGlyLeuLysTrpGluLeu  506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182  TTTGAAACCATCGCTGCCCTGGGAAATTACCACCCACGACTGGACTGAAGTGGCAGCTG  241

Qy   507  GlyArgIlePheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAsp  526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242  GGACGCAATCTTTGGCACTCTTCCTACACATTTCTTGGCCCTGATGGAT  301

Qy   527  AspValHisLeuLysLeuAlaAsnGluGluThrIleLysLysAsnIleThrHisTrpThrLeu  546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302  GATGTCCACCTCAAGCTTGCTAATGAAGAAACAATAAAGAAGAACATCACTCACTGGACTCTG  361

Qy   547  PheAsnTyrTyrAsnSerSerGlyTrpAsnGluSerValProArgProProLeuHisPro  566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362  TTTAACTATTACAACCTTCTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCT  421

Qy   567  AlaAspValProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeu  586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422  GCAGATGTGCCCCGGGGTTCTTGCTGGGAGACAGCTGTGGGCATTGAATTCATGAGGCTG  481

Qy   587  ThrValSerAspMetLeuValThrTyrIleThrIleLeuLeuGlyAspPheLeuArgAla  606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482  ACGGTGTCCGACATGCTGGTAACCTACATCACCATCCTGCTGGGGGACTTCCTACGGGCT  541

Qy   607  CysPheValArgPheMetAsnTyrCysTrpCysTrpAspLeuGluLeuAlaGlyPhe  624
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   542  TGTTTTGTCGGGTTCATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGGATTT  595
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RESULT 6
US-10-487-887-7
;   Sequence 7, Application US/10487887
;   Publication No. US20040249139A1
;   GENERAL INFORMATION:
;   APPLICANT: Griffith, Andrew J
;   APPLICANT: Kurima, Kiyoto
;   APPLICANT: Wilcox, Edward
;   APPLICANT: Friedman, Thomas
;   TITLE OF INVENTION: TRANSDUCTIN-1 AND TRANSDUCTIN-2 AND APPLICATIONS TO HEREDITARY
;   TITLE OF INVENTION: DEAFNESS
;   FILE REFERENCE: 226544
;   CURRENT APPLICATION NUMBER: US/10/487,887
;   CURRENT FILING DATE: 2004-02-26
;   PRIOR APPLICATION NUMBER: PCT/US02/29614
;   PRIOR FILING DATE: 2002-09-19
;   PRIOR APPLICATION NUMBER: 60/323,275

Alignment Scores:

Pred. No.:		
Score:	1.42e-88	Length: 3216
Percent Similarity:	99.00	Matches: 140
Best Local Similarity:	98.59%	Conservative: 0
Query Match:	98.59%	Mismatches: 0
DB:	10.93%	Indels: 1
	9	Gaps: 2
		0

US-10-792-307-4 (1-906) x US-10-792-307-7 (1-3216)

```
Qy   213 MetAlaLysLysTrpValLysPheLysArgAspPheAspAsnPheLysThrGlnCysIle 232
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   904 ATGGCTAAGAAAATGGGTCAAGTTAAGGAGGACTTTGATAATTTCAAGACTCAATGTATT 963

Qy   233 ProTrpGluMetLysIleLysAspAspIleGluSerHisPheGlySerSerValAlaSerTyr 252
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   964 CCCTGGGAAATGAAGATCAAGGACATTGAAAGTCACTTCGGTTCTTCTGTGGCATCTTAC 1023

Qy   253 PheIlePheLeuArgTrpMetTyrGlyValAsnLeuValLeuPheGlyLeuIlePheGly 272
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1024 TTCATCTTTCTCCGATGGATGTATGGAGTTAACCTTGTCCTTTTTGGCTTAATATTTGGT 1083

Qy   273 LeuValIleIleProGluValLeuMetGlyMetProTyrGlySerIleProArgLysThr 292
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1084 CTAGTCATCATCCCAGAGGTGCTGATGGGCATGCCCTATGGAAGTATACCCAGAAAGACG 1143

Qy   293 ValProArgAlaGluGluGluLys-AlaMetAspPheSerValLeuTrpAspPheGluGl 312
         |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db  1144 GTGCCTCGAGCTGAGGAAGAGCG-AGCCATGGACTTCTCTGTCCTTTGGGATTTTGAGGG 1202

Qy   312 yTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnGlnArgThrIleGlyTr 332
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1203 CTACATCAAATATTCTGCTCTCTTCTATGGCTACTACAACCACCGGACCATTGGATG 1262

Qy   332 pLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSerValPheGlyTyrSe 352
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1263 GCTGAGGTACAGGCTGCGCCATGGCTACTTTATGGTGGGGGTCAGCGTGTTTGGCTACAG 1322

Qy   352 rLeu 353
         ||||
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 23:39:38 ; Search time 588 Seconds
                                             (without alignments)
                                             479.533 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 906
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Scoring table: OLIGO
               Xgapop 60.0 , Xgapext 60.0
               Ygapop 60.0 , Ygapext 60.0
               Fgapop   6.0 , Fgapext   7.0
               Delop   6.0 , Delext   7.0

Searched: 3289935 seqs, 1556l0033 residues

Word size: 70

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xip
-
Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080817_19853/app_query.fasta_1
.1095
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2noligo.rnpbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=70
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10792307 @CGN_1_1_184_@runat_23112005_080817_19853
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_New:*
               1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
               2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
               3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
               4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
               5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
               6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
               7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
               8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
               9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
               10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES

Result   Query   e
No.   Score   Match Length DB   ID   Description
------ -----   ------------ --   --   -----------

No matches found

Search completed: December 5, 2005, 05:10:03
Job time : 589 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 22:52:13 ; Search time 7245 Seconds
                                             (without alignments)
                                             5850.807 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 906
Sequence: 1 MSHQVKGLKEEARGGVKGRV...........PSQTHPWRSASGKSAQRPH 906

Scoring table:
                 OLIGO
                 Xgapop   60.0 ,   Xgapext 60.0
                 Ygapop   60.0 ,   Ygapext 60.0
                 Fgapop   6.0 ,   Fgapext   7.0
                 Delop   6.0 ,   Delext   7.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 70

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-
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.1095
-DB=EST -QFMT=fastap -SUFFIX=p2noligo.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=70 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10792307 @CGN_1_1 8010 @runat_23112005_080815_19776 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	102	11.3	1827	10	AY406224	AY406224 Homo sapi
2	89	9.8	1827	10	AY406226	AY406226 Mus muscu
3	80	8.8	247	6	CD635963	CD635963 56089332H
c 4	80	8.8	247	6	CD635964	CD635964 56089332J

ALIGNMENTS

RESULT 1
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LOCUS   AY406224   1827 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION   Homo sapiens TMC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY406224
VERSION   AY406224.1 GI:39762198
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 1827)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE   2 (bases 1 to 1827)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
TITLE   Direct Submission
JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1827
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1..>1827
                     /gene="TMC2"

ORIGIN

/locus_tag="HCM2486"

Alignment Scores:

Pred. No.:
Score: 5.2e-92   Length: 1827
Percent Similarity: 102.00   Matches: 102
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 11.26%   Indels: 0
                          10   Gaps: 0

US-10-792-307-4 (1-906) x AY406224 (1-1827)

Qy   625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGly 644
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   979 CCTTCATATCCTGAGTTTGATATTAGTGGAAATGCTGGGTTTGATCTTCAACCAAGGA 1038

Qy   645 MetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 ATGATCTGGATGGGCTCCTTCTATGCTCCAGGGCCTGGTGGGCATTAATGTGCTGCGCCTG 1098

Qy   665 LeuThrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGC 1158

Qy   685 ValPheLysAlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPhe 704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 GTGTTCAAAGCCTCCCGATCCAACAACTTCTACATGGGCCTCCTGCTGTTGGTGCTCTTC 1218

Qy   705 LeuSerLeuLeuProValAlaLeuTyrThrIleMetSerSerLeuProProSerPheAspCysGly 724
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 CTCAGCCTCCTGCCGTGGCCTACACCATCATGTCCTCCCACCCCTCCTTTGACTGCGGG 1278

Qy   725 ProPhe 726
           ||||||
Db   1279 CCGTTC 1284

RESULT 2

LOCUS   AY406226   1827 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Mus musculus TMC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406226
VERSION   AY406226.1 GI:39762200
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1827)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios

REFERENCE   2 (bases 1 to 1827)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
COMMENT   This sequence was made by sequencing genomic exons and ordering
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                     /locus_tag="HCM2486"
ORIGIN

Alignment Scores:

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Query Match: 100.00%   Mismatches: 0
DB: 9.82%   Indels: 0
                          10   Gaps: 0

US-10-792-307-4 (1-906) x AY406226 (1-1827)

Qy   625 ProSerTyrAlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGly 644
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Db   979 CCTTCATATCCTGAGTTTGATATTAGTGGAAATGCTGGGTTTGATCTTCAACCAAGGA 1038

Qy   645 MetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeu 664
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 ATGATCTGGATGGGCTCCTTCTATGCTCCAGGGCCTGGTGGGCATTAATGTGCTGCGCCTG 1098

Qy   665 LeuThrSerMetTyrPheGlnCysTrpAlaValMetSerSerAsnValProHisGluArg 684
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 CTGACCTCCATGTACTTCCAGTGCTGGGCGGTGATGAGCAGCAACGTACCCATGAACGC 1158

Qy   685 ValPheLysAlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPhe 704
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 GTGTTAAAGCCTCCAGATCCAACAACTTCTACATGGGCCTCCTGCTGTTGGTGCTCTTC 1218

Qy   705 LeuSerLeuLeuProValAlaLeuTyrThr 713
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Db   1219 CTCAGCCTCCTGCCGTGGCCTACACC 1245

RESULT 3

LOCUS   CD635963   247 bp   mRNA   linear   EST 12-JAN-2004
DEFINITION 56089332H1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD635963

VERSION   CD635963.1 GI:40284230
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
             extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
   PUBMED   15203218
COMMENT   Contact: Fu GK
             Incyte Genomics, Inc.
             3160 Porter Dr., Palo Alto, CA 94304, USA
             Tel: 650454102
             Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
     source   1..247
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

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  Query Match: 8.83%   Mismatches: 0
  DB: 6   Indels: 0
                                           Gaps: 0

US-10-792-307-4 (1-906) x CD635963 (1-247)

Qy   361 AlaSerAsnThrGlnGlySerThrGlyGluGlyGluSerAspAsnPheThrPheSerPhe 380
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Db   8 GCCAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGGAGTGACAACTTCACATTCAGCTTC 67

Qy   381 LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr 400
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Db   68 AAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACACAGCCTGATAACAAATAT 127

Qy   401 AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnGluSerAsnLysGlu 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 GCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAGTAACAAAAGA 187

Qy   421 GluAsnIleHisLeuThrArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysCys 440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 GAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGT 247

RESULT 4
CD635964/c
LOCUS   CD635964
DEFINITION   560893232J1 FLP Homo sapiens cDNA, mRNA sequence.
             CD635964   247 bp   mRNA   linear   EST 12-JAN-2004

ACCESSION   CD635964
VERSION   CD635964.1 GI:40284231
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
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             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1 (bases 1 to 247)
  AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
  TITLE   Circular rapid amplification of cDNA ends for high-throughput
             extension cloning of partial genes
  JOURNAL   Genomics 84 (1), 205-210 (2004)
   PUBMED   15203218
COMMENT   Contact: Fu GK
             Incyte Genomics, Inc.
             3160 Porter Dr., Palo Alto, CA 94304, USA
             Tel: 650454102
             Email: gfu@incyte.com.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="FLP"
                     /note="Vector: pDrive Cloning Vector"
ORIGIN

Alignment Scores:
  Pred. No.:   1
  Score: 1.93e-70   Length: 247
  Percent Similarity: 80.00   Matches: 80
  Best Local Similarity: 100.00%   Conservative: 0
  Query Match: 8.83%   Mismatches: 0
  DB: 6   Indels: 0
                                           Gaps: 0

US-10-792-307-4 (1-906) x CD635964 (1-247)

Qy   361 AlaSerAsnThrGlnGlySerThrGlyGluGlyGluSerAspAsnPheThrPheSerPhe 380
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Db   240 GCCAGCAATACCCAAGGAAGCACAGGCGAAGGGGAGGAGTGACAACTTCACATTCAGCTTC 181

Qy   381 LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr 400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 AAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACACAGCCTGATAACAAATAT 121

Qy   401 AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnGluSerAsnLysGlu 420
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Db   120 GCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAGAGTAACAAAAGA 61

Qy   421 GluAsnIleHisLeuThrArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysCys 440
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 GAAAATATCCATCTGACAAGATTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGT 1

Search completed: December 5, 2005, 04:28:56
Job time : 7248 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:51 ; Search time 10018 Seconds
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Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Searched: 5883141 seqs, 2842172565 residues

Scoring table: BLOSUM62
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               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
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             7: gb_ph:*
             8: gb_pr:*
             9: gb_ro:*
             10: gb_sts:*
             11: gb_sy:*
             12: gb_un:*
             13: gb_vi:*
             14: gb_htg:*
             15: gb_pl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4744	100.0	3169	8	AF417580	AF417580 Homo sapi
2	3808	80.3	3216	8	AF417581	AF417581 Mus muscu
3	3139.5	66.2	3066	5	AY581309	AY581309 Gallus ga
4	2657	56.0	2566	5	AY581308	AY581308 Gallus ga
5	2566.5	54.1	1977	5	AY263168	AY263168 Takifugu
6	2384	50.3	2871	8	AY263167	AY263167 Takifugu
7	2344.5	49.4	3201	8	AF417578	AF417578 Homo sapi
8	2300	48.5	2895	9	AF417579	AF417579 Mus muscu
9	1692.5	35.7	6222	8	AY263157	AY263157 Mus muscu
10	1678.5	35.4	4746	8	AY263163	AY263163 Homo sapi
11	1675	35.3	3495	5	AY581310	AY581310 Gallus ga
12	1657.5	34.9	2442	8	AY236490	AY236490 Homo sapi
13	1640	34.6	3621	9	AY236491	AY236491 Mus muscu
14	1466	30.9	2560	8	AX833218	AX833218 Sequence
15	1466	30.9	2560	8	AK094789	AK094789 Homo sapi
16	1412	29.8	2572	2	AY263175	AY263175 Anopheles
17	1374.5	29.0	884	6	CQ728483	CQ728483 Sequence
18	1167	24.6	2276	6	CQ734586	CQ734586 Sequence
19	1138	24.0	179086	5	BX295526	BX295526 Zebrafish
20	1138	24.0	222623	14	BX950215	BX950215 Danio rer
21	1120.5	23.6	5929	6	CQ578280	CQ578280 Sequence
22	1087	22.9	222623	14	BX950215	BX950215 Danio rer
23	1072.5	22.6	1548	8	AY263169	AY263169 Takifugu
24	928.5	19.6	1528	8	AK098607	AK098607 Homo sapi
25	840.5	17.7	198392	2	CR383678	CR383678 Zebrafish
26	747.5	15.8	8770	2	AF098506	AF098506 Caenorhab
27	747.5	15.8	45097	2	U23516	U23516 Caenorhabdi
28	733.5	15.5	737	6	CQ716638	CQ716638 Sequence
29	730	15.4	418	8	AY263156	AY263156 Mus muscu
30	716	15.1	129662	5	BX950207	BX950207 Zebrafish
31	679	14.3	2738	8	AX833146	AX833146 Sequence
32	679	14.3	2738	8	AK094664	AK094664 Homo sapi
33	643.5	13.6	3581	8	AY263165	AY263165 Homo sapi
34	643.5	13.6	3581	8	BC036205	BC036205 Homo sapi
35	638.5	13.5	3504	8	AY236498	AY236498 Homo sapi
36	633.5	13.4	2384	8	BC047719	BC047719 Homo sapi
37	624	13.2	2330	9	AY236499	AY236499 Mus muscu
38	623	13.1	2932	9	AY263161	AY263161 Mus muscu
39	617.5	13.0	2465	8	AB168722	AB168722 Macaca fa
40	617.5	13.0	3013	5	AY581312	AY581312 Gallus ga
41	614	12.9	192769	5	BX571945	BX571945 Zebrafish
42	607	12.8	410	9	AY263155	AY263155 Mus muscu

43	602	12.7	2511	5	AY263173
44	560.5	11.8	2430	2	AY263177
45	547	11.5	159272	8	HSD568C3

AY263173 Takifugu
AY263177 Anopheles
AL049712 Human DNA

ALIGNMENTS

RESULT 1

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LOCUS       AF417580      3169 bp    mRNA    linear   PRI 05-MAR-2003
DEFINITION  Homo sapiens transmembrane channel-like protein 2 (TMC2) mRNA,
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ACCESSION   AF417580
VERSION     AF417580.2  GI:28642834
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 3169)
  AUTHORS   Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
            Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
            Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Riazuddin,S.,
            Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F.,
            Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
  TITLE     Dominant and recessive deafness caused by mutations of a novel
            gene, TMC1, required for cochlear hair-cell function
  JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
   PUBMED   11850618
REFERENCE   2 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
REFERENCE   3 (bases 1 to 3169)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAR-2003) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
  REMARK    Sequence update by submitter
COMMENT     On Mar 3, 2003 this sequence version replaced gi:19223982.
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                     ADVPRGSCWETAVGIEFHRLTVSDMLVTYIITLLGDFLRACEVRPMNYCWCWDLEAGE
                     PSYAEFDISGRNVLGLIFNQGMIWMGGSFYAPGLVGINVLRLLTSMYFQCMAVMSSNVPH
                     ERVFKASRSNNFYMGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFSSGKRMYDVLGETI
                     ENDPTFLGKIFAFLANPGLIIPAILMFLAIYYLNSVSKSLSRANAQLRKKIQVLRE
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ORIGIN
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US-10-792-307-4 (1-906) x AF417580 (1-3169)

Alignment Scores:

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	4744.00	Matches:	906
Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
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Qy   1 MetSerHisGlnValLysGlyLeuLysGluGluAlaArgGlyGlyValLysGlyArgVal  20
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Db   1 ATGAGCCACCAGGTAAAGGGGCTGAAAGAGGAAGCACGAGGCGGGAGTGAAAGGGCCGGTG  75

Qy  21 LysSerGlySerProHisThrGlyAspArgLeuGlyArgSerSerSerLysArgAla     40
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Db  76 AAGAGCGGCTCTCCACACACAGGTGACAGGCTGGGAAGGAGATCTCAAGCAAGCGGGGCT   135

Qy  41 LeuLysAlaGluGlyThrProGlyArgArgGlyAlaArgGlnSerGlnLysGluArgAla  60
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Db 136 CTCAAAGCCGAGGGAACCCCAGGCAGCGGCCCCGGAGCTCACGGAGCAAGCGGAAGGCGGC  195

Qy  61 GlyGlySerProSerProGlySerProProArgLysGlnThrGlyArgArgArgHisArg  80
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Db 196 GGGGGCAGCCCAAGCCCCGGGGTCTCCCCGAGGAAGCAAACAGGCGCGAGAGAGACACGA   255

Qy  81 GluGluLeuGlyGluGlnGluArgGlyGluAlaGluArgThrCysGluGlyArgArgLys  100
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Db 256 GAAGAGCTGGGCGAGCAGGAGCGGGGCGAGGCAGAGAGGACCTGCGAGGGCAGGAGGAAG   315

Qy 101 ArgAspGluArgAlaSerPheGlnGluArgThrAlaAlaProLysArgGluLysGluIle  120
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Db 316 CGCGACGAGAGGGCCTCCTTCCAGGAGCGGACAGCAGCCCCAAAAGAGGGAAAAGGAGATT  375

Qy 121 ProArgLysGluGluLysSerLysArgGlnLysLysProArgSerSerLeuAlaSer     140
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Db 376 CCGAGGAAGGAGGAGAAGTCGAACGGGCAGAAGAAACCCAGGTCATCCTCTTGGCCTCC   435
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Qy   141  SerAlaSerGlyGlySerGluGlyGluLeuAlaGlnIleLeuGluGlnVal       160
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Db   436  AGTGCCTCTGGTGGGGAGTCCCCTGTCCCAGGAGGAACTGGCCCAGATCCTGGAGCAGGTG   495

Qy   161  GluGluLysGlyLysLeuIleAlaThrMetArgSerLysProTrpProMetAlaLysLys   180
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Db   496  GAAGAAAAAAAAGAAGCTCATTGCCACCATGCGGAGCAAGCCCTGGCCCATGGCAAGAAG    555

Qy   181  LeuThrGluLeuArgGluAlaGlnGluPheValGluGlyLysTyrGluGlyLysAlaLeuGlyLys   200
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   556  CTGACAGAGCTCAGGGAGGCCCAGGAATTTGTGGAGAAGTATGAAGGTGCCTTGGGAAAG    615

Qy   201  GlyLysGlyLysGlnLeuTyrAlaTyrLysLysMetAlaLysLysTrpValLysPhe    220
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   616  GGGAAAGGCAAGCAACTATATGCCTACAAGAAGATGGCTAAGAAGTGGGTCAAATTT     675

Qy   221  LysArgAspAspAsnPheLysAspLysThrGlnIleProProGluMetLysMetAsp    240
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Db   676  AAGAGAGACTTTGATAATTTCAAGACATCAAATGTATCCCCTGGGAAATGAAGATGGAC    735

Qy   241  IleGluSerHisPheGlySerSerValAlaSerTyrPheIlePheLeuArgTrpMetTyr   260
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Db   736  ATTGAAAGTCACTTTGGTCTTCTCAGTGGCATCGTATTTCATCTTTCTCCGATGGATGTAT   795

Qy   261  GlyValAsnLeuValLeuPheGlyLeuLeuPheGlyLeuLeuIleIleIleProGluValLeu   280
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   796  GGAGTTAACCTTGTCCTTTTTGGCTTAATATTTGGTCTACTAATCCCAGAGGTACTG     855

Qy   281  MetGlyMetProTyrGlyLysSerIleProArgGlyLysThrValProArgAlaGluGluGluLys   300
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Db   856  ATGGGCATGCCCTATGGGAAGTATTCCCAGAAGACAGTGCCTCGGGGTGAGGAAGAAAAG   915

Qy   301  AlaMetAspPheSerValLeuTrpAspPheGlyTyrIleLysTyrSerAlaLeuPhe    320
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Qy   321  TyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTrpLeuArgTyrArgLeuProMetAla   340
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Qy   341  TyrPheMetValGlyValSerValPheGlyTyrSerLeuIleIleValIleArgSerMet   360
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Db  1036  TACTTTATGGTGGGGGTCAGCGTGTTCGGGTACAGCCTGATTATTGTCATTCGATCGATG  1095

Qy   361  AlaSerAsnThrGlnGlySerThrGlyGlyGlyLeuSerAspAsnPheThrPheSerPhe   380
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Db  1096  GCCAGCAAATACCCAAGGACACAGGGGAGGAGTGACACAACTTCACATTCAGCTTC     1155

Qy   381  LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrArgLeuAlaAspAsnLysTyr   400
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Db  1156  AAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACACGTGATAACAAATAT  1215

Qy   401  AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnGluSerAsnLysGlu   420
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Qy   441  LeuCysGlySerGlyTyrLeuIleTyrPheValValLysArgSerGlnPheSerLys    460
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Qy   461  MetGlnAsnValSerPheTyrGluArgAsnGluValGlyIleValValMetSerLeuGly   480
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Qy   481  MetPheCysProProLeuPheGluThrIleAlaAlaLeuGluAsnTyrHisProArgThr   500
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Qy   541  IleThrHisThrLeuPheAsnThrTyrTyrAsnSerSerGlyTrpAsnGluSerValPro   560
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Qy   681  ProHisGluArgValPheLysAlaSerArgSerAsnPheTyrMetGlyLeuLeuLeu    700
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Qy   881 ProAspProSerGlyHisAlaProSerGlnThrHisProTrpArgSerProAlaSerGlyLysSer 900
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Db  2716 GCTCAGAGACCTCCCAC 2733
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RESULT 2
AF417581

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DEFINITION  Mus musculus transmembrane channel-like protein 2 (Tmc2) mRNA,
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ACCESSION   AF417581
VERSION     AF417581.1  GI:19223984
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3216)
  AUTHORS   Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
            Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
            Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S.,
            Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F.,
            Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
  TITLE     Dominant and recessive deafness caused by mutations of a novel
            gene, TMC1, required for cochlear hair-cell function
  JOURNAL   Nat. Genet. 30 (3), 277-284 (2002)
   PUBMED   11850618
REFERENCE   2  (bases 1 to 3216)
  AUTHORS   Kurima,K., Griffith,A.J. and Friedman,T.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
            Rockville, MD 20850, USA
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                     KKLRLRLREAQAPVEKYEGALGKGRGKHLYAYRMMMAKKMWVKFKRDFDNFKTQCIPWEM
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ORIGIN
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Alignment Scores:

Pred. No.:			
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Percent Similarity:	87.50%	Conservative:	50
Best Local Similarity:	81.97%	Mismatches:	95
Query Match:	80.27%	Indels:	18
DB:	9	Gaps:	3

US-10-792-307-4 (1-906) x AF417581 (1-3216)

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(Second column)

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ORIGIN

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YFVVKRSQTFSRMQNAGWYERNEVEIVWSLLGMFCPPLFETIATLENYHPRIGLKWQL
GRIFALFLGNLYTFLLALMDDVNEKLAEEDVVKNITRWTLFGHYNSSMENSTATPAPL
DPADVPRGPCWETTVGIEIVRLTVSDILVTFVILVGDFIRACFVRMNYCWCWDLEA
GPFSYAEFDISGNVLGLVFNQGMIWMGGSFYAPGLVGINVLRLLTSMYFQCWAVMSSNV
PHARVFKASKSNNFYMGLILLILFLSLLPVAYTIMSLPPSFDCGPFSSGKKRMVDVIOE
TIELDFPLFVAKIFGYVANPGLIIPAILLMVVLAIYYLNAVSEAYQRANAELKKKMQLQ
REEENRNRNNKASTNSMMQDLEDLLAPSTKSESSPKQAEDKKKDSPNQASPVGRKOEKA
EVLNSSPIAAGRRAAFIPPPHVLVTRPLTPGTWAPYPQPRQPWPGGRPMGPFPGRGRG
QPRYIHPI"
```

US-10-792-307-4 (1-906) x AY581309 (1-3066)

```
Qy   57 LysGluArgAlaGlyGlySerProSerProGlyArgArgLysGlnThrGlyArg 76
         ::|||||||||| : |  ||||:::::           ||||:
Db  115 AAAGAAGAAAATGAGAGCAAAGACCAAGGAGAGAAAATTGTCCTCAACAAACGCAGAGCGCTCAGG 174

Qy   77 ArgArg---HisArgGluGluLeu------GlyGluGlnLuArgGlyGluAlaGluArg 93
         |||||:          |||   :::                    ||||||
Db  175 AGGAAAAAATCATCGAATGAAAAGAAAATGATGGAAAAGAAGGAGGAGGAG------- 225

Qy   94 ThrCysGluGlyArgArgLysArgGluAlaSerPheGlnLuArgThrAlaAla 113
         ||||||:::||        ||||||||:::::||||||
Db  226 ------------------AGAGAAAAAGGCTTCTTCCAAAGATGAAAAGGAGTCA 264

Qy  114 ProLysArgGlyGluLeuProLysArgLys-----------GlyGluSerLysArg 129
         ::|||||||||    |||       ||:::  |||::
Db  265 GAAAATAAGGAAAAGAGAAAGAAAAACATGAAAGGAGAAAGAGGAGGACAAGAAGAA 324

Qy  130 GlnLysGlyProArgSerSerSerLeuAlaSerGlyAlyGlySerLeuSer 149
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Db  325 GGCAGAGGAAAAACAGTGCCTCTTCCAACTCTTCCAACTCTCGACGAGAATCACTGTCA 384

Qy  150 GluGluGluLeuAlaGlnIleLeuGluGlnValGlyLuGlyLysLysLeuIleAlaThr 169
         |||||||   ::::::||||||    |||:||::||||
Db  385 GAGGAAGAGCTTCCAATGCTGATGGAAAGAGGTGGACAGAAAGAAAAAACTCATCTCCACC 444

Qy  170 MetArgSerLysProTrpProMetAlaLysLysLeuThrGluLeuArgGluAlaGlnGlu 189
         |||||||       |||   ||| ||||||:::|||||||:::
Db  445 ATGAGAAACAGCCCTGGCCAATGATGAAAAAAGCTCTCTGTGCTCAGGAGGCACAAGCT 504

Qy  190 PheValGluLysTyrGluGlyValAlaLeuGlyLysGlyLysGlnLeuTyrAlaTyr 209
         |||||||||:::|||||||||||||||:::||||||
Db  505 TTCGTTGAGAAGTTTGAGGGGACCGCCCTGGGAAAAGGGAAAAGTCTGTATGCATAT 564

Qy  210 LysMetLeuMetAlaLysTrpValLysPheValArgAspPheAspAsnPheSerThr 229
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Db  565 AAGATGATGATGGCGAAGAGTGGGTGAAATTTAAGAGAGACTTTGACAACTTCAAAACC 624
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```
Qy  230 GlnCysIleProTrpGlnMetLysValIleGluLysAspIleGluSerHisPheGlySerSerVal 249
         |||||||::::::|||||||||||:::::||||||||||||||||||
Db  625 CAGTGCATACCCTGGGAGATGAAGGTTATAAGAAGAAGAGCACTTCGGTTCCTCTTT 684

Qy  250 AlaSerTyrPheIlePheLeuArgTrpMetTyrGlyValValAsnLeuValLeuPheGlyLeu 269
         :::||||||||||||||||||:::||||||||||||||||||
Db  685 GCTTCCTATTTCATTTTCTGCGATGGATGTGTAAATCTTGTCCTTTTGGATTA 744

Qy  270 IlePheGlyLeuValIleIleLeuProGluValValLeuMetGlyMetProTyrGlySerIlePro 289
         :::||||||||||||||||||||||:::::||||||:::
Db  745 ATATTTGGACTGGTTATAATTCCAGAGGTCCTGATGGGAATGCCATATGGGAGCATCCCA 804

Qy  290 ArgLysThrValProArgAlaGlyLeuProMetAlaTyrPheMetValGlyValSerValPhe 309
         ||||||:::||||||||||||:::::||||||||||||||||||:::
Db  805 AGAAAACTGGTTAAATACAGGCCTTCCAATGGCATATTTCATGGTTGGGGTCAGTGTGTTT 864

Qy  310 PheGluGlyTyrTyrIleLysTyrSerAlaLeuPheTyrGlyTyrTyrAsnAsnGluArgThr 329
         ||||||||||:::||||||||||||:::||||||:::||||||
Db  865 TTTGAGGGGTACATCAAGTACTCAGCGCTCTTTTATGGGTACTACAACAACGAGCGGACA 924

Qy  330 IleGlyTrpProLeuArgTyrArgLeuProMetAlaLeuTyrPheMetValGlyValSerPhe 349
         |||||||||||||||||||:::|||:::||||||||||||
Db  925 ATTGGAAACCCAGAGCAGCACAGCAACAAGTTTGCATCCATCACCACCAGCTTCAAGGAA 984

Qy  350 GlyTyrSerLeuIleIleValIleArgSerMetAlaSerAsnArgGlnGlySerThrGly 369
         ||||||||||||||||||||||:::||||||:::||||||
Db  985 GGCTACAGCCTGATGGTTCGTTATAGATCGATGGCACGGAACATCCAATGAAAAGCACAGCA 1044

Qy  370 GluGlyGlySerAspAsnPheThrPheSerPheLysMetPheThrSerPheAspTyrLeu 389
         :::|||||||||||||||||||:::||||||:::||||||
Db 1045 GATGGGGACGATGACAACTTCGTTTCACCTGAAAAATGTTCACAAGCTGGGACTACCTC 1104

Qy  390 IleGlyAsnSerGluThrAlaAspAsnLysTyrAlaSerIleThrThrSerPheLysGlu 409
         ||||||:::||||||||||||||||||:::||||||||||||
Db 1105 ATTGGAAACCCAGAGACAGCAGACAACAAGTTTGCATCCATCACCACCAGCTTCAAGGAA 1164

Qy  410 SerIleValAspGluGlnIleGluSerAsnLysGluGluAsnIleHisLeuThrHisArgPheLeu 429
         ||||||||||||||||:::|||||||||||||||||:::
Db 1165 TCTATTGTGGATGAGCAAAGAGAAAGCAACATCCATCTGACGCATAGGTTTCTG 1224

Qy  430 ArgValLeuAlaAsnPheLeuIleIleCysCysGlySerGlyTyrTyrLeuTyr 449
         ||||||:::||||||:::||||||||||||||||||||||||
Db 1225 CGGGTCCTGGCCAACTCCTCATCATATGCCTGCTGTGGGAGCGGCGCTACCTCATTTAC 1284

Qy  450 PheValValLysArgSerGlnGlnPheSerLysMetGlnAsnValSerTrpTyrGluArg 469
         ||||||||||||||||||:::||||||:::||||||||||||
Db 1285 TTTGTGGTGAAACGCTCCCAGACGTTTCAAAAATGCAGAATGCTGGGTGGTATGGAGAGA 1344

Qy  470 AsnGluValGlyIleValMetSerLeuLeuGlyMetPheCysProProLeuPheGluThr 489
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Db 1345 AATGAGGTTGAAATCGTGATGTCCTTGCTGGGCATGTTTTGCCCTCCCCTGTTTGAAACT 1404

Qy  490 IleAlaAlaLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGlyArgIle 509
         |||||| ||||||:::||||||||||||:::||||||||||||
Db 1405 ATTGCCACACTGGAAAACTACCATCCACGCATCGGGCTGAAGTGGCAGCTGGGGCGCATC 1464

Qy  510 PheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuAlaLeuMetAspAspValHis 529
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Db   1465 TTTGCCTCTTCCTGGGAAACCTCACGGTTCTTCCTTCTGGCCTTGATGGATGATGTCAAC 1524
          |||||||||||||||||||||||||||||||||||||||||||||||||||||...||:||

Qy    530 LeuLysLeuAlaAsnGluGluThrIleTyrLeuAsnSerArgAlaAsnIleThrHisTrpThrLeuPheAsnTyr 549
          ||||||                          :::
Db   1525 GAAAAACTGGCTAAGAAGAGTGTTGTGAAGAACATCACCGGCGTTGGACACTGTTTGGCCAC 1584

Qy    550 TyrAsnSerSerGlyTyrTrpAsnGluSerValProArgProProLeuHisProAlaAspVal 569
          ||||||                    :::
Db   1585 TATAACTCCTCCATGGAGAACAGCGCATGCTACCCCAGCTCCCCTTCGACCCGCAGATGTG 1644

Qy    570 ProArgGlySerCysTrpGluThrAlaValGlyIleGluPheMetArgLeuThrValSer 589
          ||||||| |||:::|||
Db   1645 CCCAGGGGCAGCTGCTGGGAGACAGCAGTTGGCATTGAGATCATGAGGCTCACCGTGTCT 1704

Qy    590 AspMetLeuValThrTyrIleLeuThrIleLeuGlyAspPheLeuArgAlaCysPheVal 609
          |||:::||| |||||
Db   1705 GATATCCTGGTGACCTTCGTAACCATCCTGGTGGGAGATTTCATCCGAGCTTGCTTCGTG 1764

Qy    610 ArgPheMetAsnTyrCysTrpCysTrpAspLeuGluAlaGlyPheProSerTyrAlaGlu 629
          ||||||                  :::
Db   1765 AGATTCATGAATTACTGTTGGTGCTGGGACCTAGAGGCCGGATTTCCTTCATGCAGAG 1824

Qy    630 PheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnIleGlyMetIleTrpMetGly 649
          |||||||:::|||
Db   1825 TTTGACATCAGTGGCAACGTTTTGGGTTTGATCTTCAACCAAGGAATGATTTGGATGGGA 1884

Qy    650 SerGlyPheTyrAlaProGlyLeuValGlyIleLeuAsnValLeuArgLeuLeuThrSerMetTyr 669
          |||||||:::|||||
Db   1885 TCCTTTTATGCACCAGGTCTTGTGGGTATAAACGTGCTGCGCTTATTAACCTCCATGTAT 1944

Qy    670 PheGlnCysTrpAlaValMetSerSerAsnValProHisGluArgValPheLysAlaSer 689
          |||||||||||:::
Db   1945 TTTCAGTGCTGGGCTGTCATGAGTAGCAATGTTCCTCATGAGCGAGTATTCAAAGCATCC 2004

Qy    690 ArgSerAsnAsnPheTyrMetGlyTyrLeuLeuLeuLeuValLeuPheLeuSerLeuLeuPro 709
          |||:::|||||
Db   2005 AGTCTAAACAACTTTTACATGGGCTACCTGCTGCTGTTGGTTCTGTTCCTGTCACTCCC 2064

Qy    710 ValAlaThrTyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSerGlyLys 729
          |||:::
Db   2065 GTGGCCTACACACCATCATGTCCCTCCTTCCTTTCGACTGCGGACCATTCAGGTGGAAAG 2124

Qy    730 AsnAsnArgMetTyrAspValLeuGlnLeuThrIleGlyLysAspPheProThrPheLeuGly 749
          |||||||||||  |||:::
Db   2125 AAAAGGATGTATGATGTCATTCAAGAGACCATCGGGAAGGACTTTCCCACTTTTTTGTTGCC 2184

Qy    750 LysIlePheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleLeuLeuMetPhe 769
          |||||| ||||:::
Db   2185 AAGATCTTCGGCTATCTGGCCAATCCAGGACTAATCATTCCTGCAATTCTGCTCATGGTC 2244

Qy    770 LeuAlaIleTyrTyrLeuAsnSerValSerLeuSerArgAlaAsnAlaGlnLeu 789
          ||||||::::::||
Db   2245 CTCGCTATCTATTATCTAAATTCTGTCTCTGAAGCGTCATCAGCGCCGCCAACGCAGAGTTG 2304

Qy    790 ArgGlyLysLysIleGlnValLeuArgGluValGlySerHisLysSerValLysGlyLys 809
          |||  ::::::|||  |||
Db   2305 AGAGGAAAAATGCAACTGCAAGCTGAAGAGAAAAGAGAAAAGAGAAAAGAGAAACAAAAGCCAGC 2364
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Db   2305 AGAGGAAAAATGCAACTGCAAGCTGAAGAGAAAAGAGAAAAGAGAAAAGAGAAACAAAAGCCAGC 2364

Qy    810 AlaThrThrAla----ArgAspSerGluAspThrProGlyProSerSerLysAsnAlaThr 827
          ::: ::::||| |||||
Db   2365 ACTAATTCCATGATCCAAGATCTGGAGGATTTACTTGCACCGAGT---------------- 2409

Qy    828 GlnLeuGlnLeuThrLysGluGlnThrProProSerAlaSerGlnSerGlnAlaMet 847
          ||||||  |||:::::::|||
Db   2410 ------------ACGAGAGTGAAAAGCCTCCC-----------------AAACAAGCAGAA 2442

Qy    848 AspLysLysAlaGlnGlyProGlyThrSerAsnSerAlaSerArgAspThrArgLeuProAla 867
          |||   ||||||
Db   2443 GACAAGAAAAAAGATTCTCC---------AATCAAGCCAGCCCTGTT-------------- 2481

Qy    868 SerGlyHisIleLeuProIleSerArgProProGlyIleIleGlyProAspSerGlyHisAlaPro 887
          ||| |||||| |||
Db   2482 ---GGGAAACAAGAAA-AGCAGAAGTCCTGAACAGCAGCCCCCATAGCCGCTGGGAGGAG 2537

Qy    888 SerGlnThrHisHisProTrpArgSerAlaSerGlyLysSerAlaGlnArgArgProProHis 906
          ||| :::||| :::|||
Db   2538 AGCAGCGATTCATCCCACCCACCACGTACTGGTTGACCACGGGCCACTGACCACCAGGCAC 2594
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RESULT 4

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LOCUS       AY581308                2566 bp    mRNA    linear   VRT 31-MAY-2005
DEFINITION  Gallus gallus transmembrane channel-like 1 (Tmc1) mRNA, complete
            cds.
ACCESSION   AY581308
VERSION     AY581308.1  GI:52547954
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 2566)
  AUTHORS   Mutai,H., Mann,S. and Heller,S.
  TITLE     Identification of Chicken Transmembrane Channel-like (TMC) genes:
            Expression analysis in the cochlea
  JOURNAL   Neuroscience 132 (4), 1115-1122 (2005)
  PUBMED    15857715
REFERENCE   2  (bases 1 to 2566)
  AUTHORS   Mutai,H. and Heller,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-2004) Otolaryngology, Harvard Medical School,
            Massachusetts Eye and Ear Infirmary, Eaton-Peabody Laboratory, 243
            Charles Street, Boston, MA 02114, USA
FEATURES             Location/Qualifiers
     source          1..2566
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /chromosome="2"
                     /tissue_type="inner ear"
                     /dev_stage="embryo"
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     gene            1..2566
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                     1..2566
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CDS   1..2544
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                /gene="Tmc1"
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                /protein_id="AAT85599.1"
                /db_xref="GI:52547955"
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                RGRAGGNEGSDSEGGDPTKARKNQANQKSKEDDEGQEEDEKGKSGKGNEKKQDKKADK
                KGTKEKANKKKKDKKRKSGSGSDSDSEEEPITEEELAKLKEEVEEKKKLIATLRNKPWK
                MKKKLSVLKEAQLFVEKFEGALGKGKHKYAYXVVNMTKKWMKFQRDFENKTACIPW
                EMKIKEIESHFGSSVASYFIFLRWMYGINMILFGLTEGLVMVPEALMGKPYGSLPRKT
                VPRAEAATANNFATLWDFEGPAQYSVLFYGYYNNQRTGIMLKFRMPLSYFLVGVGTIG
                YSFMIVIRTWARNANEGGDDTSFNFSWKMFTSWDYLIGNPETAINKFASITTSFKE
                AIVEEQESRKEENIHLTRFLRVLANFLALCTLAGSYLIFFVVRRSQKFALEGLENYG
                WWERNEVNVMMSLLGMFCPTLFDVISSLENYHPRIALRWQLGRIFALFLGNLYTFIIA
                LMDEINLKLEEEKIVKYNMIWEASLYNGTIPENSTAPPIQVDPADVPRGPCWETMVG
                QEFVRLTVSDTMTTYIITILLGDFLRAVFVRRFNYCWCWDLEYGFPSYSEFDISGNVLG
                LINNQGMIWMGSFYAPCLPAINVFRLHTSMYLQGWAVMCCNVPQERVFKASRSNNFYM
                AMLLFLFLSTLPAVYTIVSIPPSFDCGPFSGKTRMFEVISETLEHDFPSWFGKVFGY
                ASNPGLIPFILLMVLSIYLNATSKSYKEANLELKKKLQTSRRKQKKK"

ORIGIN

Alignment Scores:

Pred. No.:   1
Score: 4.34e-111   2657.00
Percent Similarity: 75.968   62.52%
Best Local Similarity: 62.52%
Query Match: 56.018   5

Length: 2566
Matches: 507
Conservative: 109
Mismatches: 153
Indels: 42
Gaps: 11

US-10-792-307-4 (1-906) x AY581308 (1-2566)
DB:

Qy   13 ArgGlyGlyValLysGlyArgValLysGlySerGlySerProHisThrGlyAspArgLeuGly 32
        |||||| ::|||||||| ::: ||||||
Db 202 AGGGGACATGCCAGGAGGGAGGAGCCAGACATGGTGGTCAAGGAGAGGATGGAGAT------ 252

Qy   33 ArgArgSerSerLysArgArgAlaLeuLysAlaGlyLyThrProGlyArgGlyAla 52
        ||| | |||||||| ||::||| |||||
Db 253 ------------------------GATGAAGATGGGACA-----AGGAGCTGGG 279

Qy   53 GlnArgSerGlnLysGluArgAlaGly--- 64
        |||||::: ||| ||| |||||||
Db 280 CAACGACGAGGAGAACCGGAGGGAGCTGGAGCGACGGTGGAAATGAGGGCAGTGAT 339

Qy   65 SerProGlySerPro-------ArgArgLysGlnThrGlyArgArg---ArgHisArg 80
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Db 340 TCTGAGGGGGATCCTACAAAAGCGGAGGAGAACCAGCGAAATCAAAAATCAAAGGAAGAT 399

Qy   81 GluGluLeuGlyLeuGlyIleArgGlyValuGlyIleArgThrCysGluGlyValGlyLys 100
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Db 400 GATGAACAAGAGAGATGAAAAAGGGGTAAGAGTGGGAAAGGCAAAAATGAGAAGAA 459

Qy 101 ArgAspGluArgAlaSerPheGlnArgThrAlaAlaProLysArgGlyLysGluIle 120
        :::||:|::|||:::|||||| ::|| |||||||||||::|
Db 460 CAGGACAAAAAGGCTGAT----------------AAGAAAGGGACA 489

Qy 121 ProArgLysGluGluLysSerArgGlnLysGlyLysSerProArgGlySerSerLeuAlaSer 140
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Db 490 AAAGAAAAAGGCCCAACAAGAAGAAAAAGGACAAAAAG---AAATCAGGATCTGGCTCTGAT 546

Qy 141 SerAlaSerGlyGlyValGluLeuSerGluGluLeuAlaGlnIleLeuGlnVal 160
        ||| ::::|||||||||||||||||||::: ||
Db 547 TCTGACTCTGAGGAGGAGCCGATTACTGAGGAGGAATTGGCAAAGCTGAAAGAAGAGGTA 606

Qy 161 GluGluLysLysLysGluGluLysSerArgGlnLysGluLysTrpProMetAlaLys 180
        |||||||||||| ::|||||||| |::||::|||| ||::||||||
Db 607 GAAGAAAAAAAGAAGGCTAATTGCCACGTTACGAAATAAGCCATGGAAGATGAAAAGAG 666

Qy 181 LeuThrGluLeuArgGluValPheValGlnLysValGlyLysAlaLeuGlyLys 200
        ||::: ||||||||||||||||::: ||||||||||||||||||||||||||
Db 667 TTGTCAGTTCTCAAAAGAAGCAGAGCTTTTTGTTGAAAAATTGAAAGGTGGTCTTGGAAAA 726

Qy 201 GlyGlyGlyLysGlyGlnLeuThrTyrLysMetLeuMetAlaLysLysTrpValValPhe 220
        ||||||||||||::: ||||||||||||||||||:::||||||||||||:::
Db 727 GGGAAGGGAAAAAAGTTCATCCATACAAGAGTGATGATGACCAAGAAAATGGAAATTC 786

Qy 221 LysArgAspAspPheAlaAspAsnPheLysThrGlnCysIleProTrpGluMetLysIleLysAsp 240
        :::|||||||::||||||||||||||||||||||||||::|||||::|||||||
Db 787 CAAAGAGATTTTGAGAATTTTAAGACAGCCTGCATACCCTGGGAAATGAAAATTAAAGAG 846

Qy 241 IleGluSerHisPheGlySerSerValAlaSerTyrPheIlePheLeuArgTrpMetTyr 260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 847 ATTGAAAGTCACTTTGGCTCATCGGTAGCATCTTATTTCATATTCTTACGCTGGATGTAT 906

Qy 261 GlyValAsnLeuIleLeuPheGlyLeuLysIleProGluValLeu 280
        ||||||||||||||||||||||||||||:::::||||||||||
Db 907 GGAATAAACATGATTCTCTTTGGACTTGACGTTTGAAATTGCCTGAGGCGTTTG 966

Qy 281 MetGlyMetProTyrGlySerIleProArgLysThrValProArgAlaGluGluValLys 300
        |||||| ::||| ||::|| ::::|||||| ||||||
Db 967 ATGGGAAAGCCATATGGCTCTTTACCTGAGAAAACTGTTCCAAGAGCTGAAGAAGTTACG 1026

Qy 301 AlaMetAspPheSerValLeuTrpAspPheGluGlyTyrIleLysTyrSerAlaLeuPhe 320
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Db 1027 GCTATGAACTTGCTACTCTTTGGGGATTTAGTGGGTATATCAAGTATTCTGTGGCTTTTT 1086

Qy 321 TyrGlyTyrTyrAsnAsnGlnArgThrIleGlyTyrArgLeuProMetAla 340
        ||||||||||||||||||||||||||||||::: | :::||||||||||
Db 1087 TATGGCTATTACTAATAATCAGAGGACAATTGATGGGCGTCAAGTTCAGGATGCCTTTCC 1146

Qy 341 TyrPheMetValGlyValSerValPheGlyTyrSerLeuIleIleValIleArgSerMet 360
        ||||||||||||||||||||||||||||||||::::::||||||||||||||::||||
Db 1147 TATTTCCTTGTTGGTGGTCAGCGTATTTGGCTACAGCTTTATCATTGTCATTCGAAGCATG 1206

Qy 361 AlaSerAsnThrGlnGlySerThrGlyGlyGluSerAspAsnPheThrPheSerPhe 380
        ||| |||||| |||||||||||||||||::: ||||||||||:::
Db 1207 GCAAGGAATGCA---AATGAAGAAGGTGGTGGGGATACTAGCTTTAATTTCAGCTGG 1263

Qy 381 LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr 400
        ||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 1264 AAAATGTTCACAAGCTGGGACTACCTGATTGGCAATCCTGAGACAGCAGATAATAAGTTT 1323

Qy 401 AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnLeuSerAsnLysGlu 420
         |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db 1324 GCTTCTATCACTACCAGCTTTAAGGAGAGCATCGTGGAGGAGGAGGCCGAAAGGAG 1383

Qy 421 GluAsnIleHisLeuThrArgPheLeuArgValLeuLeuAlaAsnPheLeuIleIleCysCys 440
         |||||:|||||||||||||||||:|||||||||||||||||||||||::|||
Db 1384 GAAAATATTCACTTGACTCGGTTCCTGAGGGTTCTTGCTAACTTCTTAGCCCTGCACA 1443

Qy 441 LeuCysGlySerGlyTyrLeuIleTyrPheValValLysArgSerGlnGlnPheSer--- 459
         ||||||||||||||||||||||||||||::|||||||||||||||||:::
Db 1444 CTTGCTGGGAGGTGGCTACCTCATATTTTTTGTGTGAGGAGATCCCAGAAATTTGCCCTG 1503

Qy 460 ---LysMetGlnAsnValSerTrpTyrGluArgAsnGluValGluIleValMetSerLeu 478
         :::::||||||||||||||||||||||||||||||||||||||:|:|||||
Db 1504 GAAGGTCTGGAGAACTACGGGTGGTGGGAAAGAAATGAAGTAAACATGGTCATGTCACTT 1563

Qy 479 LeuGlyMetPheCysProProLeuPheGluThrIleAlaAlaLeuGluAsnTyrHisPro 498
         |||||||||||||||||||||:||||||||||||::||||||||||||:::
Db 1564 TTGGGAATGTTCTGTCCACCTTGTTTGATGTTATCAGTTCTCTGGAAAACTACCATCCT 1623

Qy 499 ArgThrGlyLeuLysTrpGlnArgIlePheAlaLeuPheLeuGlyAsnLeuTyr 518
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Db 1624 CGAATAGGTCTTAAGATGGCAGCTCGGACCGCCATATTTGCTCTTTTCCTGGCAAATCTAT 1683

Qy 519 ThrPheLeuLeuAlaLeuMetAspAspValHisLeuLysLeuAlaAsnGluGluThrIle 538
         :::::||||||||||||||||||||||||||||||||| :::
Db 1684 ACTTTCATTATTGCCCTAATGGATGAAAATCAATCTCAAGTTGGAAGAAGAAAGATAGTC 1743

Qy 539 Lys---AsnIleThrHisTrpThrThrLeuPheAsnTyrTyrAsnSerSerGlyTrpGluThr 557
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Db 1744 AAGTATAAACATGACAATATGGGAAGCCAGTCTTCGACAGTGTACAATGGCACTATTCCAGAAAATTCA 1803

Qy 558 SerValProArgProProLeuHisProAlaAspValProArgGlySerCysTrpGluThr 577
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Db 1804 ACTGGCTCCGCCAATTCAGGTGGACCCTGCAGAGTCTCCAGAGTGTTGGGAAACA 1863

Qy 578 AlaValGlyIleGluPheMetArgLeuThrValSerAspMetLeuValThrTyrIleThr 597
         ||||||||||||||||||||||||||||||||||||::
Db 1864 ATGGTAGGCCAGAATTTGTACGGCTGACAGTCTCTGACACGATGACAACATATATCACA 1923

Qy 598 IleLeuLeuGlyAspPheLeuArgAlaCysPheValArgPheMetAsnTyrCysTrpCys 617
         |||||||::||||||||||||||||||||| |||||||||||||||
Db 1924 ATTCTAATTGGGTGACTTCTTGAGAGCTGTCTTTGTTAGGTTTTTCAATTACTGCTGGTGC 1983

Qy 618 TrpAspLeuGluAlaGlyPheProSerTyrAlaGluPheAspIleSerGlyAsnLeu 637
         |||||||||| |||||||
Db 1984 TGGGACTTGGAAATATGGATTTCCATCATATTCAGAGTTTGATATAAGTGGGAATGTCTC 2043

Qy 638 GlyLeuIlePheAsnGlnGlyMetIleTrpMetGlySerPheTyrAlaProGlyLeuVal 657
         |||||||| ||||||||||||||| |||
Db 2044 GGACTGATATTTAACCAAGGCATGATCTGGATGGGATCTTTTTATGCTCCATGTCCCA 2103

Qy 658 GlyIleAsnValLeuArgLeuLeuThrSerMetTyrPheGlnCysTrpAlaValMetSer 677
         ||||||||||||| ||||||||||||||||||||||||
Db 2104 GCAATCAAATGTGTTCCGACTACTTCAATGTACCTGCAAATGCTGGGAGTCAGTGATGTGC 2163

Qy 678 SerAsnValProHisGluArgValPheLysAlaSerArgSerAsnAsnPheTyrMetGly 697

OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 4, 2005, 17:37:51 ; Search time 1128 Seconds
                                           (without alignments)
                                           5353.024 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext   0.5
                Ygapop 10.0 , Ygapext   0.5
                Fgapop   6.0 , Fgapext   7.0
                Delop   6.0 , Delext   7.0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_21:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4642	97.8	3121	8	Acc69914	Acc69914 Human tra
2	4325.5	91.2	5027	5	Aas92296	Aas92296 DNA encod
3	3808	80.3	3216	8	Acc69616	Acc69616 Mouse tra
4	2344.5	49.4	4333	8	Acc69613	Acc69613 Human tra
5	2300	48.5	2895	8	Acc69615	Acc69615 Mouse tra
6	1619	34.1	3357	13	Adu01837	Adu01837 Novel hum
7	1466	30.9	2560	11	Adm01657	Adm01657 Human cDN
8	1456.5	30.7	3897	13	Adu01668	Adu01668 Novel hum
9	1227	25.9	2591	6	Abv75613	Abv75613 Human rib
10	1120.5	23.6	5929	4	Abl05865	Abl05865 Drosophil
11	679	14.3	2738	11	Adm01585	Adm01585 Human cDN
12	538	11.3	3566	13	Adr07551	Adr07551 Full leng
13	519	10.9	2357	13	Adq87039	Adq87039 Human tum
14	517.5	10.9	2358	6	Acn92177	Acn92177 Breast ca
15	516	10.9	2355	6	Abz23382	Abz23382 Nucleotid
16	516	10.9	2355	6	Abz23383	Abz23383 Reverse c
17	515	10.9	2403	3	Aaf81776	Aaf81776 Human mem
18	499.5	10.5	2321	3	Aaa16626	Aaa16626 Human sec
19	493	10.4	11963	6	Abl05864	Abl05864 Drosophil
20	486	10.2	2001	6	Abz11813	Abz11813 Human pol
21	486	10.2	2001	12	Adm44331	Adm44331 Novel hum
22	473.5	10.0	2824	14	Ady17129	Ady17129 DNA encod
23	472.5	10.0	2629	10	Ade95583	Ade95583 Human NOV
24	465.5	9.8	4572	10	Add69632	Add69632 Human REM
25	457.5	9.6	2902	6	Abq54905	Abq54905 Human ova
26	449.5	9.5	2399	11	Adm03417	Adm03417 Human cDN
27	449.5	9.5	3256	9	Acc48561	Acc48561 Transmemb
28	449.5	9.5	3285	11	Adn39932	Adn39932 Cancer/an
29	449	9.5	3696	10	Ada09906	Ada09906 Human rec
30	447.5	9.4	2203	10	Ade95581	Ade95581 Human NOV
31	446	9.4	2433	12	Adg67421	Adg67421 Human tum
32	442	9.3	2418	8	Acc48786	Acc48786 Human Evi
33	442	9.3	2420	8	Acc48790	Acc48790 Human Evi
34	442	9.3	2420	8	Acc48791	Acc48791 Human Evi
35	439.5	9.3	3812	10	Adi21979	Adi21979 Novel hum
36	437.5	9.2	2389	8	Acc48788	Acc48788 Human Evi
37	434	9.1	2057	10	Adi21987	Adi21987 Novel hum
38	428.5	9.0	1839	14	Aeb56941	Aeb56941 Human pol
39	428.5	9.0	2389	8	Acc48792	Acc48792 Human Evi
40	422.5	8.9	2421	9	Acc48570	Acc48570 TMDC part
41	418	8.8	5357	12	Adg86636	Adg86636 Human tum
42	355	7.5	2131	9	Acc59891	Acc59891 Human REM
43	338	7.1	1804	13	Adp23695	Adp23695 PRO polyp
44	338	7.1	1804	13	Adu06103	Adu06103 Novel bro

ALIGNMENTS

RESULT 1
ACC69614
ID   ACC69614 standard; cDNA; 3121 BP.
XX
AC   ACC69614;
XX
DT   18-JUL-2003 (first entry)
XX
DE   Human transduction-2 (TDC2) encoding cDNA SEQ ID NO:3.
XX
KW   Human; transduction-2; TDC2; hearing loss; auditory; gene therapy; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
FH
FH   Key   Location/Qualifiers
FT
FT   CDS   16..2688
FT   /*tag= a
FT   /product= "transductin-2"
XX
SQ   Sequence 3121 BP; 778 A; 823 C; 824 G; 696 T; 0 U; 0 Other;

CC   and/or mutant TDC1 or TDC2 gene obtained from the animal; (4) a method
CC   for treating an animal prophylactically or therapeutically for hearing
CC   loss due to a complete or partial loss of wild type TDC1 or TDC2; and (5)
CC   a method for identifying one or more agents that interact with a TDC1
CC   and/or TDC2 genes in a cell by administering one or more agents to the
CC   cell comprising the genes and assaying the expression level of the genes
CC   by the cell, where an increase or decrease in the expression level is
CC   indicative of the interaction between the agents and the genes in the
CC   cell. TDC1 and TDC2 have auditory activities and can be used in gene
CC   therapy. The molecules, compositions and methods of the present invention
CC   can be used for prognosticating, treating and monitoring hearing loss

Alignment Scores:
Pred. No.:   Length: 3121
Score: 4642.00   Matches: 890
Percent Similarity: 98.23%   Conservative: 0
Best Local Similarity: 98.23% Mismatches: 0
Query Match: 97.85%   Indels: 16
DB: Gaps: 1

US-10-792-307-4 (1-906) x ACC69614 (1-3121)

Qy   1 MetSerHisGlnValLysGlyLeuLysGluGluAlaArgGlyGlyValLysGlyArgVal 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16 ATGAGCCACCAGGTAAAAGGGCTGAAAGAGGAA------------------------ 48

Qy   21 LysSerGlySerProHisThrGlyAspArgLeuGlyArgSerSerLysArgAla 40
          ||||||||||||||||||||||||||||||||||
Db   49 ----------------GGTGACAGGCTGGGAAGGAGATCCTCAAGCAAGCGGGCT 87

Qy   41 LeuLysAlaGluGlyThrProGlyArgArgGlyAlaGlnArgSerGlnLysGluArgAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 CTCAAAGCCGAGGGGACACCCAGCAGGGCGCGGAGCTCACGCAAGCCCAGAAGGAGCGCGCC 147

Qy   61 GlyGlySerProSerProGlySerProArgArgGlyGlnThrGlyArgArgArgHisArg 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 GGGGGCAGCCCAAGCCCGGGTCTCCCCGGAGGAAGCAAAACAGGGCGCGAGGAGACAGA 207

Qy   81 GluGluLeuGluLysGlnGluGlnArgThrCysGlyGlyArgArgLys 100
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   208 GAAGAGCTGGGGAAGCAGGAGCAGCGGACGTGCGGAGGGCAGGAGGAAAG 267

Qy   101 ArgAspProLeuArgGlnAlaSerPheGlnGluArgThrAlaAlaProLysArgGlyLysGluIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 CGCGACGAGCAGGGGCCTCCTTCCAGGAGCAGCGGGACAGCAGCCCCAAAAGAGGGAAAAGAGATT 327

Qy   121 ProArgLysGluGluValLysSerArgGlnIleLysProArgSerSerSerLeuAlaSer 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 CCGAGGAAGGAAGAGAGAAGTCAGAAGCAGCAGAAGAAACCCAGGTCATCCTTGGCCTCC 387

Qy   141 SerAlaSerGlyGlyGluSerLeuSerGlnGluGluGluGlnIleLeuGlnIleLeuGlnValVal 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AGTGCCTCTGGTGGGGAGTCCCTGTCCGAGGAGGAGGAACTGGCCCAGATCCTGGAGCAGGTG 447

Qy   161 GluGluLysLysLysLeuIleAlaThrMetArgSerLysProTrpProMetAlaLysLys 180

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                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448  GAAGAAAAAAGAAGAGCTCATTGCCACCATGCGGAGCAAGCCCTGGCCGCCCATGGGAAGAAG   507
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181  LeuThrGluLeuArgGluValAlaGlnPheValGlyLysTyrGluLeuGlyLys             200
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508  CTGACAGAGCTTCAGGGAGGCCCAGGAATTTGTGGGAAGTATGAAGCTGGGAAAG             567

Qy    201  GlyLysGlyLysGlnLeuTyrArgLysTyrAlaTyrLysMetLeuMetAlaLysLysTrpValLysPhe  220
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568  GGGAAAGGCAAGCAACTATATCGCAAGTATGCCTACAAGATGCTGATGGCCAAGAAATGGGTCAAATTT  627

Qy    221  LysArgAlaAspPheAlaAsnPheLysThrGlnGlnCysIleProTrpGluMetIleLysLysAsp   240
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628  AAGAGAGCAGACTTTGCAAATTTCAAGACTCAAAATGTATCCCCTGGGAAAATGAGATCAAGGAC     687

Qy    241  IleGluSerHisPheGlySerSerValAlaSerTyrPheIleProPheLeuArgTrpMetTyr     260
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    688  ATTGAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATCCCTTCCGATGGATGTAT         747

Qy    261  MetGlyMetProTyrGlySerIleProArgLysThrValProArgAlaGluGluValLeu       280
                              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    748  GGAGTTAACCTTTGTCCTTTTGGCTTAATATTTGGTCTAGTCATTTGGTCATAAATCCCAGAGGTACTG 807

Qy    281  GlyValAlaSerLeuValLeuPheGlyLeuLeuValIleLeuIleProProLeuGluProGluValLeu  300
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    808  ATGGGCCATGCCCTTATGGGAGTATTCCCAGAAAAGACAGTGCCTCGGGCTGAGGAAGAAG       867

Qy    301  AlaMetAspPheSerValLeuTrpAspAspPheGluGlyTyrIleTyrIleLeuTyrSerAlaLeuPhe  320
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    868  GCCATGGATTTTTCGTCCTTGGGATTTGAGGGCTATATCTACAAGCTACTGCACTCTTC         927

Qy    321  TyrGlyTyrTyrAsnAsnGlnAsnGlnThrIleGlyTyrProLeuArgTyrArgGlnLeuProMetAla  340
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    928  TATGGCTACTACAACAACCAGAGACCAATCGGGCATCCGGGCTGGCTGAGGTACCGTATGGCT     987

Qy    341  TyrPheMetValGlyTyrValSerValPheGlyTyrSerLeuIleIleValIleLeuAlaArgSerMet  360
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    988  TACTTTATGGTCGGGTATGTGTCGGTCTTACAGCCTGATTATTGTCATTCGATCCATG         1047

Qy    361  AlaSerAsnThrGlnGlySerThrGlyGlyLysGluSerAspAsnPheThrPheSerPhe         380
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1048  GCCAGCAATACCCAAGGAAGCACAGGAGGGAAGGGAGAGTGACAACTTCACATTCAGCTTC       1107

Qy    381  LysMetPheThrSerTrpAspTyrLeuIleGlyAsnSerGluThrAlaAspAsnLysTyr        400
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108  AAGATGTTCACCAGCTGGGACTACCTGATCGGGAATTCAGAGACAGCTGATAACAAATAT       1167

Qy    401  AlaSerIleThrThrSerPheLysGluSerIleValAspGluGlnLeuSerAsnLysGlu        420
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1168  GCATCCATCACCACCAGCTTCAAGGAATCAATAGTGGATGAACAAAGAGTAACAAGAA        1227

Qy    421  GluAsnIleHisLeuThrArgPheLeuArgValLeuAlaAsnPheLeuIleIleCysCys          440
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228  GAAAATCCATCATCTGACAGAATTCTTCGTGTCCTGGCAACTTTCTCATCATCTGCTGT        1287

Qy    441  LeuCysGlySerGlyTyrLeuIleTyrPheValValLysArgSerGlnGlnPheSerLys        460
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228  GAAAATCCATCATCTGACAGAATTCTTCGTGTCCTGGCAACTTTCTCATCATCTGCTGT        1287
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Db   1288  TTGTGTGGAAGTGGGTACCTCATTTACTTTGTGGTTAAGCGATCTCAGCAATTCTCCAAA       1347

Qy    461  MetGlnAsnValSerTrpTyrGluArgAsnGluValGluIleValMetSerLeuLeuGly        480
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1348  ATGCAGAATGTCAGCTGGTATGAAAGGAATGAGGTTGAGATCGTGATGTCCCTGCTTGGA       1407

Qy    481  MetPheCysProProLeuPheGluThrIleAlaAlaLeuGluAsnTyrHisProArgThr        500
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1408  ATGTTTTGTCCCCCTCTGTTTGAAACCATCGGTGCCCTGGAGAATTACCACCCGCGCACT       1467

Qy    501  GlyLeuLysTrpGlnLeuGlyArgIlePheHisAlaLeuPheLeuGlyAsnLeuTyrThrPhe       520
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1468  GGACTGAAGTGGCAGCTGGGACGCATCTTTGCACTTCCTGGGGAACCTCTACACATTT        1527

Qy    521  LeuLeuAlaLeuMetAspAspAspValHisIleLeuLeuValLeuAlaAsnGluGluThrIleLysAsn  540
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1528  CTCTTGGCCCTGATGGATGACGTTCCACCTCAAGCTTGCTAATGAACAATAAAGAAGAC        1587

Qy    541  IleThrHisTrpThrLeuPheHisAsnTyrTyrAsnSerSerGlyTrpAsnGluSerValPro       560
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1588  ATCACTCACTGGACTCTGTTTAACTACTATAACAGCTCTGGTTGGAACGAAAGTGTCCCC       1647

Qy    561  ArgProProLeuHisProAlaAspAspValProArgGlySerTrpCysSerTrpGluThrAlaValGly  580
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1648  CGACCACCCCTGCACCCTGCAGATGTGCCCCGGGGTTCTTGGTGTTGGGAAGACAGCTGTGGGC    1707

Qy    581  IleGluPheMetMetArgLeuThrValSerAspAspMetLeuValThrTyrIleThrIleLeuLeu     600
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1708  ATTGAATTCATGATGCGCCTGACGGTGTCTGACGATATGCTGGTAACCTACATCACCATTCTGCTG  1767

Qy    601  GlyAspPheLeuGluArgLeuAlaCysPheValArgPheMetAsnTyrCysSerTrpCysSerTrpAspLeu 620
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1768  GGGGACTTCCTAGAGCGCCTGGTTTGTTTTGTGCGGTTCATGAACTACTGCTCGTGGGACTTG    1827

Qy    621  GluAlaGlyPheProSerTyrAlaGluGluPheAspIleSerGlyAsnValLeuGlyLeuIle        640
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Db   1828  GAGGCTGGATTCCCTTCATATGCTGAGGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATC   1887

Qy    641  PheAsnGlnGlyMetIleTrpMetGlySerPheTyrAlaProGlyLeuValGlyIleAsn         660
                              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1888  TTCAACCAAGGAATGATCTGGATGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAAT       1947

Qy    661  ValLeuArgLeuSerMetTyrPheGlnCysTrpAlaValAlaMetSerSerAsnVal          680
                              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1948  GTGCTGCGGCTCTCCATGTACTTCCAGTGCTGGGCCGTGGCGATGAGCAGCAACGTA          2007

Qy    681  ProHisGluArgValPheGluAlaSerArgAsnAsnPheTyrMetGlyLeuLeu             700
                              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2008  CCCCATGAACGGGTCTTTGAAGCCTCCAGAAACAACTTCTACATGGGCCTCCTG             2067

Qy    701  LeuValLeuPheLeuSerLeuLeuProValAlaLeuTyrThrLeuMetSerLeuProProSer     720
                              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068  CTGGTGCTTCCTCTGGCCTCCCTGCTGCCTGTGGCCCTCTACACCATCATGTCCCTCCCCTCC    2127

Qy    721  PheAspCysGlyProPheSerGlyLysAsnArgMetTyrAspValLeuGlnThrIle          740
                              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128  TTTGACTGCGGGCCGTTCAGTGGGAAAAACAGAATGTACGATGTGCTCCAAGAGACCATT       2187
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Qy    741 GluAsnAspPheProThrPheLeuGlyLysIlePheAlaPheLeuAlaAsnProGlyLeu 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 GAAAACGATTTCCAACCTTCCTGGGCAAGATCTTTGCTTTCCTCGGCAATCCAGGCCTG 2247

Qy    761 IleIleProAlaIleLeuMetPheLeuValAlaIleTyrTyrLeuAsnSerValSerLys 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 ATCATCCCAGCCATCCTGCTGATGTTCTTGGCCATTTACTACCTGAACTCAGTTTCCAAA 2307

Qy    781 SerLeuSerArgAlaAsnAlaAsnLeuArgLysLysIleGlnValLeuArgGluValGlu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AGCCTTTCCCGAGCTAATGCCAACCTGAGGAAGAAAATCCAAGTGCTCCGTGAAGTTGAG 2367

Qy    801 LysSerHisLysSerValLysGlyLysAlaThrAlaAlaArgAspSerGluAspThrProLys 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 AAGAGTCACAAATCTGTAAAAGGCAAAGCCACACCAGCAGAGATTCAGAGACACCTAAA 2427

Qy    821 SerSerSerGlyLysAsnAlaThrGlnLeuGlnLeuThrThrProProSer 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 AGCAGCTCAAAAATGCCACCCAGCTCCAACTCACCAAGGAAGAGACACCTTCCCCCTCT 2487

Qy    841 AlaSerGlnSerGlnIleAlaMetAspLysLysAlaGlnGlyProGlyThrSerAsnSerAla 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 GCCAGCCAAAGCCAGGGCCATGGACAAGAAGGCCCAGGGCCCTGGGACCTCCAATTCTGCC 2547

Qy    861 SerArgThrThrLeuProHisLeuProIleSerArgArgProProGlyIleGly 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 AGCAGGACACACTGCCTCGCTCTGGACACCTTCCTATATCTCGGCCCCTGGAATCGGA 2607

Qy    881 ProAspSerGlyHisAlaProSerGlnThrHisProThrArgSerAlaSerGlyLysSer 900
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 CCAGATTCTGGCCACGCCCCATCTCAGACTCATCCGTGGAGGTCAGCCCTCTGGAAAGAGT 2667

Qy    901 AlaGlnArgProProHis 906
          ||||||||||||||||||
Db   2668 GCTCAGAGACCTCCCCAC 2685
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RESULT 2

```
AAS92296

ID   AAS92296 standard; cDNA; 5027 BP.
XX
AC   AAS92296;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #28100.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG28109.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 28100; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5027 BP; 1316 A; 1289 C; 1339 G; 1083 T; 0 U; 0 Other;
XX
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Alignment Scores:
Pred. No.:                              2.85e-295
Score:                                  4325.50
Percent Similarity:                     89.70%
Best Local Similarity:                  88.64%
Query Match:                            91.18%
DB:
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US-10-792-307-4 (1-906) x AAS92296 (1-5027)

Length:         5027
Matches:        843
Conservative:   10
Mismatches:     17
Indels:         81
Gaps:           5
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Qy     22 SerGlySerProHis------ThrGlyAspArgLeuGlyArgArgSerSerSerLysArg 39
             |||      :::|||| |||||||||||||||||||||||||||||||||||||||
Db     25 GCTGGTCTCGAACACCTGACCTCAGGTGGGAAGGAGAGATCCTCAAGCAAGCGG 84

Qy     40 AlaLeuLysAlaGluGlyThrProGlyArgArgGlyAlaGlnArgArgSerGlnLysGluArg 59
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Db   85 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 144
Qy   85 GCCTCTCAAACCCAGGGGACGGGCCAGGGCCCGAGCCTCAGCGAAAGCCAGAAGGAGCGGC 144

Db   60 AlaGlySerProSerProGlySerProArgArgLysGlnThrGlyArgArgHis 79
Qy   60 GCCGGGGGGGCGGGGCAGCCCAACCCCGGGCGGTCTCCCCGGAGGAGGCAGAAAGCCGGCGGAGACAC 145

Db   80 ArgGluGluLeuGluGlyLnGlnArgGlyGlyLysArgThrCysGluGlyArgArg 99
Qy   80 AGAGAAGAGCTGGGGGGGACGGCCAGGAGCCCGAGGCGGGGGAGCAGAGAGGGCCAGGAGGCCAGGAGA 205

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Db 120 IleProArgLysGluGluGlyLysLysProArgSerSerSerLeuAla 139
Qy 120 ATTCCAGGAAGGAGGAGAAGAAGCCAGAAGAAACCCGGAGCAGCAGCCTGGCC 325

Db 140 SerSerAlaSerGlyGlyGluSerLeuSerGluLeuLeuUlaUlaGlnIleLeuGluGln 159
Qy 140 TCCAGTGCCTCTGGTGGGGAGTCCCTGTCTGAGCTGCTAGCAGCCCAGATCCTGGAGCAG 385

Db 160 ValGluGluGlyLysLysLeuIleAlaThrMetArgSerGlyAsnGluLysSerProCysMetAlaLys 179
Qy 160 GTGGAAGAAAAAAAAGAAGCTCATCGCCACCATGCGGAGCGGGAACGAAAAGTCCCCATGCATGGCAAAG 445

Db 180 LysLeuThrGluLeuArgGluUlaGlnGluGlyLysTyrGluGlyValAlaLeuGly 199
Qy 180 AAGCTGACAGAGCTCAGGGAGGCCCAGGAATTTGTTGGAGAAGTATGAAGGCGGCCTTGGGA 505

Db 200 LysGlyLysGlyLnLeuTyrAlaTyrLysLysMetLeuMetAlaLysSerTrpValLys 219
Qy 200 AAGGGAAAAGGCCAAGCAACTATATGCCTACAAGAAGATGCTGATGGCCCAAGAAATGGGTCAAA 565

Db 220 PheLysArgAspPheAspAsnPheLysThrGlnCysIleProTrpGluMetLysIleLys 239
Qy 220 TTTAAGAGAGACTTTGATAATTTCAAGACTCAATGTATCCCCTGGGAAATGAAGATCAAG 625

Db 240 AspIleGluSerHisPheGlySerValAlaSerTyrPheIleProPheLeuArgTrpMet 259
Qy 240 GACATTGAAAGTCACTTTGGTTCTTCAGTGGCATCGTATTTCATCCTTTCCGATGATG 685

Db 260 TyrGlyValAsnLeuPheGlyIleLeuValIleIleIleProGluVal 279
Qy 260 TATGGAGTTAACCTTGTCTTTTTTGGGTCTAGTTCATTAATCCCAGAGGAT 744

Db 280 LeuMetGlyMetPro 289
Qy 280 GTCTAGGTGATCCCTGAGGAACCCTCAGTTATGCTGCAGGAGCTGGCTGGCAAGGCCCCA 805

Db 290 ArgLysThrValProArgAlaGluValGluGlyLysAlaGluMetAspPheSer 305
Qy 290 CGGAAGACAGTTTATGTACTTCTCTTCCAACACTGGA 865

Qy 305 CTG 903

Db 904 TCCTACGGGTCTAGGTTTTGACCAAGGCTACAATTATCTTGAGGCTGAACTGAAGAAGATC 963

Db 305 -- 305

Db 964 CGGCTTCCAAGCTCACTCACATGGCTACTGCGGACATCTCAGGAGATACAATTTCAAGCTTA 1023

Db 306 ValLeuTrp--------- 308

Db 1024 CTCACGTGGCTTCTGGCAGGCCTCAGAAAATCTGCTTCCAACCTTACTTATGTGGGGTTT 1083

Qy 309 ---AspPheGluGlyTyrIleTyrSerAlaLeuPheTyrGlyTyrTyrAsnGln 327
Db 1084 CCCAAGGTTCAGGGCTATATCAAGTACTCTGCACTCTTCTATGGCTACTACAACAACCAG 1143

Db 328 ArgThrIleGlyTyrLeuArgTyrArgLeuProMetAlaTyrPheMetValGlyValSer 347
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Qy 348 ValPheGlyGlyTyrSerLeuIleIleIleValIleArgSerMetAlaSerAsnThrGlnGlySer 367
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Qy 368 ThrGlyGlyTyrSerLeuSerAspAsnPheThrPheSerPheLeuSerAspAsnGluGlnLysAsnLysValGluGlu 387
Db 1264 ACAGGCGAAGGGGAGAGTGACAACTTCACATTCAGCTTCAAGAGTTCACCAGCTGGGAAC 1323

Qy 388 TyrLeuIleGlyValAsnSerGluThrAlaLeuAspAsnLysTyrAlaSerIleGluThrSerPhe 407
Db 1324 TACCTGATCGGGAAATTCAGAGACAGCTGATTAACAAATATGCATCACCACAGCTTC 1383

Qy 408 IleGluTyrPheValValSerArgGlnGlnPheSerLysMetGlnAsnValSerTrpTyr 427
Db 1384 ATTTACTTTGTGTGGTTAAGGCAATCTCAGAATGTCAACTGGTAT 1443

Qy 428 PheLeuArgValLeuAlaAsnPheLeuIleIleIleCysCysLeuCysGlySerGlyTyrLeu 447
Db 1444 TTTCTTCGTGTCCTGGCCAACTTTCTCATCATCTGCTGTTTGTGTGGAAGTGGGTACCTC 1503

Qy 448 IleGluValGlnGlnPheSerLysMetGlnAsnValSerTrpTyr 467
Db 1504 ATTTACTTTGTGTGGTTAAGGCAATCTCAGAATGTCAACTGGTAT 1563

Qy 468 GluArgAsnGlyValGlyIleValMetSerLeuLeuGlyMetPheCysProProLeuPhe 487
Db 1564 GAAAGGAATGAGGTAGGAATCGTGATGTCCCTGCTTGGAATGTTTTGTCCCCTCTGTTT 1623

Qy 488 GluThrIleAlaAlaArgLeuGluAsnTyrHisProArgThrGlyLeuLysTrpGlnLeuGly 507
Db 1624 GAAACCATCGCTGCCCTGGAGAATTACCACCCACGAACTGGACTGAAGTGGCAGCTGGGA 1683

Qy 508 ArgIleProPheAlaLeuPheLeuGlyAsnLeuTyrThrPheLeuLeuUlaLeuLeuMetAspAsp 527
Db 1684 CGGATCTTTGCACTCTTCCTGGGGAACCTCTACACATTTCTCTTGGCCCTGCTGATGGAC 1743

Qy 528 ValHisLeuLysSerLeuAlaAsnGlyIleThrIleLysAsnIleThrHisThrProLeuPhe 547
Db 1744 GTCCACCTCAAGTCTCTAATGAACGGAACAATAAAGAACATCACTCACTGGACTCTGTTT 1803

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Qy    548  AsnTyrTyrAsnSerGlyTrpAsnGluSerValProArgProLeuHisProAla    567
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Db   1804  AACTATTACAACTCTTCTGGTTGGAACGAGAGTGTCCCCCGACCACCCCTGCACCCTGCA  1863

Qy    568  AspValProArgGlySerCysTrpGluThrAlaValGlyIleGlyPheMetArgLeuThr    587
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1864  GATGTGCCCCGGGGTTCTTGCTGGGAGACAGCGTGGGCATTGGATTCATGAGGCTGACG  1923

Qy    588  ValSerAspMetLeuValThrTyrIleThrIleLeuLeuGlyLeuPheLeuArgAlaCys    607
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1924  GTGTCTGACATGCTGGTAACGTACATCACCATCCTGCTGGGGGGACTTCCTTAGGGCTTGT  1983

Qy    608  PheValArgPheMetAsnTyrCysTrpCysTrpAspLeuGluAlaLeuGlyPheProSerTyr    627
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1984  TTTGTGCGGTTCATGAACTACTGCTGGTGCTGGGACTTGGAGGCTGAGTTTCCTTCATAT  2043

Qy    628  AlaGluPheAspIleSerGlyAsnValLeuGlyLeuIlePheAsnGlnGlyMetIleTrp    647
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Db   2044  GCTGAGTTTGATATTAGTGGAAATGTGCTGGGTTTGATCTTCAACCAAGAAATGATCTGG  2103

Qy    648  MetGlySerPheTyrAlaProGlyLeuValGlyIleAsnValLeuArgLeuLeuThrSer    667
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Db   2104  ATGGGCTCCTTCTATGCTCCAGGCCTGGTGGGCATTAATGTGCTGCGGCTGCTGACCTCC  2163

Qy    668  MetTyrPheGlnCysTrpProAlaValMetSerSerAsnValProHisGluArgValPheLys    687
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Db   2164  ATGTACTTCCAGTGCTGGCCGGTGATGAGCAGCAACGTACCCCATGAACGGGTGTTCAAA  2223

Qy    688  AlaSerArgSerAsnAsnPheTyrMetGlyLeuLeuLeuLeuValLeuPheLeuSerLeu    707
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Qy    708  LeuProValAlaTyrThrIleMetSerLeuProProSerPheAspCysGlyProPheSer    727
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Db   2284  CTGCCGGTGGCCTACACCATCATGTCCCTGCCACCTTCCTTTGACTGCGGGCCGTTCAGT  2343

Qy    728  GlyLysAsnArgMetTyrAspValLeuGlnGlyThrIleGluAsnAspPheProThrPhe    747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2344  GGGAAAAACAGAATGTACGATGTCCTCCAGAGACCATTGAAAACGATTCCCAACCTTC  2403

Qy    748  LeuGlyLysIlePheAlaPheLeuAlaAsnProGlyLeuIleIleProAlaIleLeuLeu    767
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Db   2404  CTGGGCAAGATCTTTGCTTTCCTCGCCAATCCAGGCCTGATCATCCCAGCCATCCTGCTG  2463

Qy    768  MetPheLeuValIleLeuTyrLeuAsnSerValSerLeuSerArgAlaAsnAla    787
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Db   2464  ATGTTCTTGCCANTTTACTACCTGAACTCAGTTTCCAAAAGCCTTCCGAGCTAATGCC  2523

Qy    788  GlnLeuArgLysLysIleGlnGlnValLeuArgGlnValGlnLysSerHisLysSerValLys    807
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2524  CAGCTGAGGAAGAAAATCCAAGTGCTCCGTGAAGTTGAGAAGTCACAAAATCTGTAAAA  2583

Qy    808  GlyLysAlaThrAlaArgAspSerGluAspThrProLysSerSerSerLysAsnAlaThr    827
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Db   2584  GGCAAAGCCACCGCAAGGGATTCGAGGACCACAACCTAAAAGCAGCTCCAAAAAATGCCACC  2643

Qy    828  GlnLeuGlnLeuThrLysGluGluThrThrProProSerAlaSerGlnSerGlnAlaMet    847
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Db   2644  CAGCTCCAACTCACCAAGGAAGAAGAACACTCCTCCCTCTGCCAGCCAAAGCCAGGCCATG  2703

Qy    848  AspLysLysAlaGlnGlyProGlyThrSerAsnSerArgThrThrLeuProAla    867
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2704  GACAAGAAGGCCGCAGGGCCCTGGGACCTCCAATTCTGCCAGCGAGGACCACACTGCCTGCC  2763

Qy    868  SerGlyHisLeuProIleSerArgProProGlyIleGlyProAspSerGlyHisAlaPro    887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2764  TCTGGACACCTTCCTATATCTCGGCCCCCTGGAATCGGAACCAGATTCTGGCCACGCCCCA  2823

Qy    888  SerGlnThrHisProTrpArgSerAlaSerGly    898
           |||||||||||||||||||||||||||||||||
Db   2824  TCTCAGACTCATCCGTGGAGACAGGGCCTGGGC  2856

Search completed: December  4, 2005, 20:52:13
Job time : 1226 secs
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:51 ; Search time 382 Seconds
(without alignments)
4215.892 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV.........PSQTHPWRSASGKSAQRPPH 906

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
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.1095
-DB=issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a

SUMMARIES

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1		486	10.2	2001	3	US-10-799-451-695	Sequence 695, App
2		330.5	7.0	2387	3	US-10-104-047-1902	Sequence 1902, Ap
3		177	3.7	1434	3	US-09-902-540-4356	Sequence 4356, Ap
4		177	3.7	23694	3	US-09-902-540-1216	Sequence 1216, Ap
5		170.5	3.6	1827	3	US-09-270-767-1308	Sequence 1308, Ap
6		170.5	3.6	1827	3	US-09-270-767-16590	Sequence 16590, A
7	c	168.5	3.6	54033	3	US-09-949-016-12091	Sequence 12091, A
8	c	168.5	3.6	54033	3	US-09-949-016-14325	Sequence 14325, A
9		167.5	3.6	5539	3	US-08-628-829-3	Sequence 3, Appli
10		167	3.5	73519	3	US-09-270-767-16344	Sequence 16344, A
11		167	3.5	105519	3	US-09-949-016-11769	Sequence 11769, A
12		165.5	3.5	705	3	US-09-270-767-5061	Sequence 5061, Ap
13		165.5	3.5	705	3	US-09-270-767-20343	Sequence 20343, A
14		163	3.4	1835	3	US-09-216-393B-80	Sequence 80, Appl
15		163	3.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
16		160.5	3.4	936	3	US-09-270-767-4464	Sequence 4464, Ap
17		160.5	3.4	936	3	US-09-270-767-19746	Sequence 19746, A
18		158	3.3	98567	3	US-09-949-016-11750	Sequence 11750, A
19		158	3.3	100567	3	US-09-949-016-16934	Sequence 16934, A
20		158	3.3	194937	3	US-09-949-016-17032	Sequence 17032, A
21		158	3.3	194937	3	US-09-949-016-17033	Sequence 17033, A
22		157	3.3	276687	3	US-09-949-016-13840	Sequence 13840, A
23		157	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
24	c	156.5	3.3	156651	3	US-09-949-016-17349	Sequence 17349, A
25		154.5	3.3	5253	3	US-09-423-890-7	Sequence 7, Appli
26		154.5	3.3	390890	3	US-09-949-016-14720	Sequence 14720, A
27		154	3.2	851	3	US-09-270-767-8286	Sequence 8286, Ap
28		154	3.2	851	3	US-09-270-767-23568	Sequence 23568, A
29		154	3.2	43414	3	US-09-949-016-12839	Sequence 12839, A
30		154	3.2	43415	3	US-09-949-016-16491	Sequence 16491, A
31		153	3.2	236474	3	US-09-949-016-13418	Sequence 13418, A
32		152	3.2	165651	3	US-09-949-016-13032	Sequence 13032, A
33		151.5	3.2	172251	3	US-09-949-016-15841	Sequence 15841, A
34		151.5	3.2	6789	3	US-09-269-446D-43	Sequence 43, Appl
35		150.5	3.2	90541	3	US-09-759-359A-3	Sequence 3, Appli
36		150.5	3.2	90541	3	US-09-759-973-3	Sequence 3, Appli
37		150.5	3.2	767677	3	US-09-949-016-12147	Sequence 12147, A
38		150.5	3.2	767677	3	US-09-949-016-17361	Sequence 17361, A
39		150	3.2	6644	3	US-08-875-435B-5	Sequence 5, Appli
40		149	3.1	268449	3	US-09-949-016-17244	Sequence 17244, A
41		148.5	3.1	5962	9	5386025-5	Patent No. 5386025
42		148.5	3.1	6755	3	US-09-931-999-4	Sequence 4, Appli
43		148.5	3.1	247781	3	US-09-949-016-14193	Sequence 14193, A
44		147.5	3.1	3538	3	US-09-902-540-528	Sequence 528, App
45		147	3.1	1298	3	US-08-948-705-3	Sequence 3, Appli

Search completed: December 4, 2005, 21:28:01
Job time : 3768 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:54 ; Search time 1464 Seconds
                                              (without alignments)
                                              5117.525 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Scoring table: BLOSUM62
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                 Ygapop   10.0 , Ygapext   0.5
                 Fgapop   6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 9793542-seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 listing first 45 summaries

Command line parameters:
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-MODEL=frame+_p2n.model -DEV=xlp
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-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10792307 @CGN 1.1.1549 @runat 23112005_080713_19227 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4744	100.0	3169	9	US-10-792-307-3	Sequence 3, Appli
2	4642	97.8	3121	8	US-10-487-887-3	Sequence 3, Appli
3	4326.5	91.2	4895	6	US-10-1115-831-134	Sequence 134, App
4	4325.5	91.2	5027	6	US-10-450-763-28100	Sequence 28100, A
5	3808	80.3	3216	8	US-10-487-887-7	Sequence 7, Appli
6	3808	80.3	3216	8	US-10-792-307-7	Sequence 7, Appli
7	2344.5	49.4	4333	8	US-10-487-887-1	Sequence 1, Appli
8	2344.5	49.4	4333	9	US-10-792-307-1	Sequence 1, Appli
9	2300	48.5	2895	8	US-10-487-887-5	Sequence 5, Appli
10	2300	48.5	2895	6	US-10-792-307-5	Sequence 5, Appli
11	1466	30.9	2560	6	US-10-108-260A-342	Sequence 342, App
12	1120.5	23.6	5929	10	US-11-097-143-6038	Sequence 6038, Ap
13	679	14.3	2738	5	US-10-108-260A-270	Sequence 270, App
14	517.5	10.9	2338	5	US-10-198-846-13327	Sequence 13327, A
15	515	10.9	2403	3	US-09-965-529-73	Sequence 73, Appl
16	515	10.9	2403	3	US-09-969-680A-73	Sequence 73, Appl
17	515	10.9	2403	10	US-11-048-692-73	Sequence 73, Appl
18	499.5	10.5	2321	3	US-09-374-046A-17	Sequence 17, Appl
19	499.5	10.5	2321	5	US-10-616-263-17	Sequence 17, Appl
20	493	10.4	11963	10	US-11-097-143-6037	Sequence 6037, Ap
21	486	10.2	2001	7	US-10-302-172-695	Sequence 695, App
22	472.5	10.0	2629	7	US-10-309-290-115	Sequence 115, App
23	465.5	9.8	4572	9	US-10-495-148-61	Sequence 61, Appl
24	457.5	9.6	2902	6	US-10-264-049-785	Sequence 785, App
25	449.5	9.5	2399	8	US-10-108-260A-2102	Sequence 2102, Ap
26	449.5	9.5	3256	8	US-10-487-752-2	Sequence 2, Appli
27	449.5	9.5	3285	6	US-10-295-027-1150	Sequence 1150, Ap
28	447.5	9.4	2203	7	US-10-309-290-113	Sequence 113, App
29	428.5	9.0	1839	6	US-10-945-678-17	Sequence 17, Appl
30	422.5	8.9	2421	8	US-10-487-755-11	Sequence 11, Appl
31	330.5	7.0	2387	8	US-10-104-047-1902	Sequence 1902, Ap
32	328	6.9	1330	9	US-10-945-678-6	Sequence 6, Appli
33	322.5	6.8	2452	9	US-10-945-678-30	Sequence 30, Appl
34	322.5	6.8	2452	5	US-10-450-763-10529	Sequence 10529, A
35	298	6.3	2384	6	US-10-108-260A-1066	Sequence 1066, Ap
36	297.5	6.3	1140	5	US-10-264-237-220	Sequence 220, App
37	287.5	6.1	1060	5	US-10-027-632-122322	Sequence 122322,
38	287.5	6.1	1060	6	US-10-027-632-122322	Sequence 122322,
39	280.5	5.9	2290	8	US-10-643-795A-11	Sequence 11, Appl
40	280.5	5.9	2290	9	US-10-948-518-11	Sequence 11, Appl
41	250	5.3	600	9	US-10-972-079-86723	Sequence 86723, A
42	245.5	5.2	1194	8	US-10-357-930-22456	Sequence 22456, A
43	245.5	5.2	1194	8	US-10-357-930-25672	Sequence 25672, A
44	245.5	5.2	1194	8	US-10-357-930-28291	Sequence 28291, A
45	245	5.2	599	9	US-10-972-079-86722	Sequence 86722, A

Search completed: December 4, 2005, 23:18:01
Job time : 1573 secs

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 20:26:42 ; Search time 231 Seconds
              (without alignments)
              1220.629 Million cell updates/sec

Title: US-10-792-307-4
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSOTHPWRSASGKSAQRPPH 906

Scoring table: BLOSUM62
              Xgapop 10.0 , Xgapext 0.5
              Ygapop 10.0 , Ygapext 0.5
              Fgapop 6.0 , Fgapext 7.0
              Delop   6.0 , Delext   7.0

Searched: 3289935 seqs, 15561 0033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model - DEV=xlp
Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080714_19253/app_query.fasta_1
.1095
-DB=Published Applications NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10792307_@CGN_1_1_184_@runat_23112005_080714_19253
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG - DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published Applications NA_New:*
  1: /cgn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq:*
  2: /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*
  3: /cgn2_6/ptcdata/1/pubpna/US07_NEW_PUB.seq:*
  4: /cgn2_6/ptcdata/1/pubpna/US08_NEW_PUB.seq:*
  5: /cgn2_6/ptcdata/1/pubpna/PCT_NEW_PUB.seq:*
  6: /cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
  7: /cgn2_6/ptcdata/1/pubpna/US11_NEW_PUB.seq:*
  8: /cgn2_6/ptcdata/1/pubpna/US11_NEW_PUB.seq2:*
  9: /cgn2_6/ptcdata/1/pubpna/US11_NEW_PUB.seq3:*

SUMMARIES

	Result No.	Score	% Query Match	Match Length	DB	ID	Description
c	1	191	4.0	1559	6	US-10-750-185-45753	Sequence 45753, A
c	2	178.5	3.8	1611	6	US-10-750-185-52663	Sequence 52663, A
c	3	178	3.8	1177	7	US-11-102-240-129	Sequence 129, App
	4	155.5	3.3	5468	6	US-10-821-234-49	Sequence 49, Appli
	5	154.5	3.3	5253	9	US-11-004-057-3	Sequence 3, Appli
	6	149.5	3.2	5233	7	US-11-060-914-1	Sequence 1, Appli
	7	144.5	3.0	5073	6	US-10-909-125-827	Sequence 827, App
	8	138.5	2.9	2492	6	US-10-821-233-629	Sequence 629, App
	9	137.5	2.9	177623	7	US-11-112-908-41	Sequence 41, Appl
	10	135.5	2.9	1359	6	US-10-821-234-305	Sequence 305, App
	11	135	2.8	150468	7	US-11-112-908-56	Sequence 56, Appl
	12	135	2.8	193789	7	US-11-112-908-55	Sequence 55, Appl
	13	126.5	2.7	161994	7	US-11-112-908-57	Sequence 57, Appl
	14	126	2.7	1152	7	US-11-147-360-1	Sequence 1, Appli
	15	122.5	2.6	179892	7	US-11-112-908-39	Sequence 39, Appl
c	16	122	2.6	1869	7	US-11-147-360-3	Sequence 3, Appli
	17	122	2.6	2031	7	US-11-135-855-5	Sequence 5, Appli
	18	122	2.6	2154	7	US-11-135-855-6	Sequence 6, Appli
	19	121	2.6	79528	6	US-10-276-233A-6	Sequence 6, Appli
	20	120	2.5	3513	6	US-10-858-730-142	Sequence 142, App
	21	120	2.5	6941	6	US-10-432-483-49	Sequence 49, Appl
	22	120	2.5	756	7	US-11-135-855-15	Sequence 15, Appl
	23	119.5	2.5	2158	6	US-10-909-125-805	Sequence 805, App
	24	119	2.5	2310	7	US-11-073-579-1	Sequence 1, Appli
	25	118.5	2.5	8424	6	US-10-821-234-47	Sequence 47, Appl
	26	117.5	2.5	1836	6	US-10-467-657-3987	Sequence 3987, Ap
	27	117.5	2.5	3156	7	US-11-112-908-22	Sequence 22, Appl
c	28	117	2.5	172147	7	US-11-112-908-23	Sequence 23, Appl
	29	117	2.5	188682	6	US-11-112-908-46845	Sequence 46845, A
	30	116	2.4	2129	6	US-10-750-185-46845	Sequence 46845, A
	31	116	2.4	2848	7	US-11-060-914-3	Sequence 3, Appli
	32	116	2.4	5212	6	US-10-909-125-817	Sequence 817, App
c	33	116	2.4	8651	6	US-10-432-483-48	Sequence 48, Appl
c	34	116	2.4	1619	6	US-10-821-234-10	Sequence 10, Appl
	35	115.5	2.4	3132	6	US-10-392-234A-33	Sequence 33, Appl
	36	115	2.4	159497	7	US-11-112-908-61	Sequence 61, Appl
	37	115	2.4	5946	7	US-10-374-954-22	Sequence 22, Appl
	38	115	2.4	5997	6	US-10-374-954-20	Sequence 20, Appl
	39	114.5	2.4	7027	6	US-10-374-954-1	Sequence 1, Appli
	40	114.5	2.4	7027	6	US-10-374-954-3	Sequence 3, Appli
	41	114.5	2.4	157224	7	US-11-112-908-51	Sequence 51, Appl
c	42	114.5	2.4	159660	7	US-11-112-908-43	Sequence 43, Appl
c	43	114.5	2.4	170189	7	US-11-112-908-50	Sequence 50, Appl
c	44	114	2.4	1377	6	US-10-618-320A-2	Sequence 2, Appli
c	45	114	2.4	3305	7	US-11-017-550-68	Sequence 68, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 17:37:51 ; Search time 7246 Seconds
                                          (without alignments)
                                          5850.000 Million cell updates/sec

Title:
Perfect score: 4744
Sequence: 1 MSHQVKGLKEEARGGVKGRV..........PSQTHPWRSASGKSAQRPPH 906

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop 6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10792307/runat_23112005_080712_19179/app_query.fasta_1
.1095
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10792307 @CGN 1 1 8010 @runat_23112005_080712_19179 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
           1:   gb_est1:*
           2:   gb_est2:*
           3:   gb_est3:*
           4:   gb_htc:*
           5:   gb_est4:*
           6:   gb_est5:*
           7:   gb_est6:*
           8:   gb_est7:*
           9:   gb_gss1:*
          10:   gb_gss2:*
          11:   gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1682	35.5	11482	4	HSM806678	BX640632 Homo sapi
2	973	20.5	1827	10	AY406224	AY406224 Homo sapi
3	932	19.6	740	5	BU262560	BU262560 603374338
4	723	15.2	1827	10	AY406226	AY406226 Mus muscu
5	670.5	14.1	822	11	DQ030264	DQ030264 Homo sapi
6	656	13.8	595	11	DQ031957	DQ031957 Homo sapi
7	652	13.7	1656	4	AK016832	AK016832 Mus muscu
8	645	13.6	959	5	BY716506	BY716506 Mus muscu
9	644	13.6	657	2	BB614713	BB614713 BB614713
10	643	13.6	2435	4	AK077146	AK077146 Mus muscu
11	628.5	13.2	633	10	AY404862	AY404862 Homo sapi
12	625.5	13.2	822	11	DQ030265	DQ030265 Pan trogl
13	622.5	13.1	63	10	AY404864	AY404864 Mus muscu
14	618	13.0	419	2	BF544940	BF544940 UI-R-C2p-
15	615	13.0	4496	4	AK083189	AK083189 Mus muscu
16	599.5	12.6	633	10	AY404863	AY404863 Pan trogl
17	591.5	12.5	4523	4	CR933669	CR933669 Homo sapi
18	584	12.3	644	2	BB624822	BB624822 BB624822
19	580	12.2	450	3	BM482906	BM482906 535995 MA
20	574	12.1	513	11	DQ031958	DQ031958 Pan trogl
21	571.5	12.0	1092	8	DN708339	DN708339 CLJ76-F12
22	560	11.8	627	2	BB617044	BB617044 BB617044
23	556	11.7	2708	4	BC077431	BC077431 Xenopus l
24	538	11.3	676	1	BB024587	BB024587 BB024587
25	530	11.2	829	6	BH399926	BH399926 AG-ND-127
26	519	10.9	2319	4	CR605550	CR605550 full-leng
27	510.5	10.8	2204	4	AK050105	AK050105 Mus muscu
28	508	10.7	876	9	CC071886	CC071886 CSU-K33r.
29	508	10.7	1245	10	CL641086	CL641086 CH213-400
30	483	10.2	2721	4	AK016573	AK016573 Mus muscu
31	463.5	9.8	3906	4	AK028404	AK028404 Mus muscu
32	454.5	9.6	625	10	BX144254	BX144254 Danio rer
33	452.5	9.5	1171	10	CL645372	CL645372 CH213-93I
34	452	9.5	563	3	BP370498	BP370498 BP370498
35	449.5	9.5	2283	11	DQ049496	DQ049496 Homo sapi
36	439.5	9.3	739	7	CK471553	CK471553 AGENCOURT
37	435.5	9.2	790	7	CR853633	CR853633 DKFZp469H
38	434	9.1	3597	4	CR749359	CR749359 Homo sapi
39	429	9.0	2866	4	AK090179	AK090179 Mus muscu
40	416	8.8	247	6	CD635963	CD635963 Mus muscu
41	416	8.8	247	6	CD635964	CD635964 56089332H
42	411	8.7	2802	4	AK077671	AK077671 Mus muscu
43	407	8.6	639	9	BH376597	BH376597 AG-ND-169
44	393	8.3	597	11	DE054410	DE054410 Oryzias l
45	389	8.2	1648	11	DQ046311	DQ046311 Homo sapi

Search completed: December 4, 2005, 22:52:07

Job time : 7280 secs